Rec'd 10089057 040302

FORM PTO-1390 (Modified) (REV 11-2000) U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371

ATTORNEY'S DOCKET NUMBER: **221519US0PCT**

U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR): **10/089057**

INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/JP00/06913	**4 October 2000**	**4 October 1999 (earliest)**

TITLE OF INVENTION

GENES FOR HEAT RESISTANT ENZYMES OF AMINO ACID BIOSYNTHETIC PATHWAY DERIVED FROM THERMOPHILIC CORYNEFORM BACTERIA

APPLICANT(S) FOR DO/EO/US

Seiko HIRANO et al.

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This is an express request to begin national examination procedures (35 U.S.C. 371(f)). The submission must include itens (5), (6), (9) and (24) indicated below.
4. ☒ The US has been elected by the expiration of 19 months from the priority date (Article 31).
5. ☒ A copy of the International Application as filed (35 U.S.C. 371 (c) (2))
   a. ☐ is attached hereto (required only if not communicated by the International Bureau).
   b. ☒ has been communicated by the International Bureau.
   c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☒ An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)).
   a. ☒ is attached hereto.
   b. ☐ has been previously submitted under 35 U.S.C. 154(d)(4).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371 (c)(3))
   a. ☐ are attached hereto (required only if not communicated by the International Bureau).
   b. ☐ have been communicated by the International Bureau.
   c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
   d. ☒ have not been made and will not be made.
8. ☐ An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371 (c)(4)).
10. ☐ An English language translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371 (c)(5)).
11. ☐ A copy of the International Preliminary Examination Report (PCT/IPEA/409).
12. ☒ A copy of the International Search Report (PCT/ISA/210).

Items 13 to 20 below concern document(s) or information included:

13. ☒ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
14. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
15. ☐ A **FIRST** preliminary amendment.
16. ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
17. ☐ A substitute specification.
18. ☐ A change of power of attorney and/or address letter.
19. ☐ A computer-readable form of the sequence listing in accordance with PCT Rule 13ter.2 and 35 U.S.C. 1.821 - 1.825.
20. ☐ A second copy of the published international application under 35 U.S.C. 154(d)(4).
21. ☐ A second copy of the English language translation of the international application under 35 U.S.C. 154(d)(4).
22. ☐ Certificate of Mailing by Express Mail
23. ☒ Other items or information:

Notice of Priority/ Form PTO-1449
PCT/IB/304/ Drawings (15 sheets)
PCT/IB/308/ Sequence Listing (123 sheets)

U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR	INTERNATIONAL APPLICATION NO.	ATTORNEY'S DOCKET NUMBER
10/089057	PCT/JP00/06913	221519US0PCT

24. The following fees are submitted:.	CALCULATIONS PTO USE ONLY	
BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)) :		
☐ Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO **$1040.00**		
☒ International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO **$890.00**		
☐ International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO **$740.00**		
☐ International preliminary examination fee (37 CFR 1.482) paid to USPTO but all claims did not satisfy provisions of PCT Article 33(1)-(4) **$710.00**		
☐ International preliminary examination fee (37 CFR 1.482) paid to USPTO and all claims satisfied provisions of PCT Article 33(1)-(4) **$100.00**		
ENTER APPROPRIATE BASIC FEE AMOUNT =	**$890.00**	
Surcharge of **$130.00** for furnishing the oath or declaration later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492 (e)).	**$0.00**	

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	80 - 20 =	60	x	$18.00	**$1,080.00**
Independent claims	32 - 3 =	29	x	$84.00	**$2,436.00**
Multiple Dependent Claims **(check if applicable).**				☒	**$280.00**

TOTAL OF ABOVE CALCULATIONS =	**$4,686.00**	
☐ Applicant claims small entity status. See 37 CFR 1.27). The fees indicated above are reduced by 1/2.	**$0.00**	
SUBTOTAL =	**$4,686.00**	
Processing fee of **$130.00** for furnishing the English translation later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492 (f)). +	**$0.00**	
TOTAL NATIONAL FEE =	**$4,686.00**	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31) **(check if applicable).** ☐	**$0.00**	
TOTAL FEES ENCLOSED =	**$4,686.00**	
	Amount to be: refunded	$
	charged	$

a. ☒ A check in the amount of **$4,686.00** to cover the above fees is enclosed.

b. ☐ Please charge my Deposit Account No. _____ in the amount of _____ to cover the above fees. A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. **15-0030** A duplicate copy of this sheet is enclosed.

d. ☐ Fees are to be charged to a credit card. **WARNING:** Information on this form may become public. **Credit card information should not be included on this form.** Provide credit card information and authorization on PTO-2038.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

Surinder Sachar
Registration No. 34,423

22850

Surinder Sachar
SIGNATURE

Norman F. Oblon
NAME

24,618
REGISTRATION NUMBER

April 3 2002
DATE

Docket No.221519US0PCT

IN THE UNITED STATES PATENT & TRADEMARK OFFICE

IN RE APPLICATION OF: : ATTN: BOX SEQUENCE

SEIKO HIRANO ET AL :

SERIAL NO. 10/089,057 :

FILED:APRIL 03, 2002 :

FOR:GENES FOR HEAT RESISTANT ENZYMES OF AMINO ACID BIOSYNTHETIC PATHWAY DERIVED FROM THERMOPHILIC CORYNEFORM BACTERIA

PRELIMINARY AMENDMENT AND STATEMENT

ASSISTANT COMMISSIONER FOR PATENTS
WASHINGTON, D.C. 20231

SIR:

Responsive to the Office Communication dated July 17, 2002, Applicants submit a substitute Sequence Listing and a corresponding computer-readable Sequence Listing.

IN THE SPECIFICATION

Please amend the specification as follows.

Page 111 (Abstract), after the last line, beginning on a new page, please replace the original Sequence Listing with the substitute Sequence Listing attached hereto.

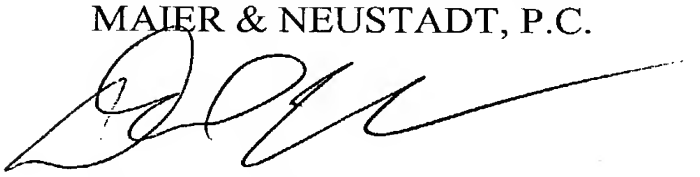
REMARKS

Applicants have now submitted a substitute Sequence Listing and a corresponding computer-readable Sequence Listing. The sequence information recorded in the corresponding computer-readable Sequence Listing is identical to the paper copy of the substitute Sequence Listing. Support for all of the sequences listed in the substitute Sequence Listing is found in the present application as originally filed. No new matter is believed to have been introduced by the submission of the substitute Sequence Listing and the corresponding computer-readable Sequence Listing.

Applicants submit that the present application is ready for examination on the merits. Early notice to this effect is earnestly solicited.

Respectfully submitted,

OBLON, SPIVAK, McCLELLAND,
MAIER & NEUSTADT, P.C.



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Specification

Genes for Heat resistant Enzymes of Amino Acid Biosynthetic Pathway Derived from Thermophilic Coryneform Bacteria

Technical Field

The present invention relates to heat resistant enzyme genes, in particular, genes for enzymes of biosynthetic pathway and uptake system of L-amino acids such as L-glutamic acid, of *Corynebacterium thermoaminogenes*, which is a thermophilic coryneform bacterium.

Background Art

The current main stream of the production of L-amino acids such as L-glutamic acid is the fermentative production utilizing coryneform bacteria. As for the fermentative production of L-amino acids, it has been attempted to reduce the cost based on breeding of strains with superior productivity and development of fermentation techniques. Although conventional attempts for realizing the cost reduction were mainly directed to achieving higher yield, energy required for cooling the fermentation heat generated during the culture cannot be ignored in addition to the raw material as the factors concerning the fermentation cost. That is, as for usual

microorganisms used for the fermentation, the temperature of the medium rises due to fermentation heat generated by the microorganism themselves during the fermentation, and hence enzymes required for the fermentation may be inactivated or the productive bacteria may be killed. Therefore, it is necessary to cool the medium during the fermentation. Accordingly, in order to reduce the cooling cost, fermentation at high temperatures has been studied for many years. Moreover, if high temperature fermentation becomes possible, the reaction rate may also be improved. However, as for the L-amino acid fermentation, effective high temperature culture has not been realized so far.

Corynebacterium thermoaminogenes is a bacterium classified into coryneform bacteria like *Corynebacterium glutamicum* (*Brevibacterium lactofermentum*), which is commonly used for the fermentation of L-amino acids. However, it shows the optimum growth temperature of 37-43°C, which is higher than that of *Corynebacterium glutamicum*, i.e., 30-35°C, and shows the optimum temperature for L-glutamic acid production of 42-45°C, which is considerably shifted to the high temperature region (Japanese Patent Laid-open (Kokai) No. 63-240779/1988).

Meanwhile, there have been developed techniques for enhancing L-amino acid producing ability of *Corynebacterium* and *Brevibacterium* bacteria by

introducing a gene coding for an L-amino acid synthesis system enzyme derived from *Escherichia coli* or *Corynebacterium glutamicum* into them. Examples of such an enzyme include, for example, citrate synthase (Japanese Patent Publication (Kokoku) No. 7-121228/1995), which is an enzyme of the L-glutamic acid biosynthetic pathway, glutamate dehydrogenase (Japanese Patent Laid-open No. 61-268185/1986), isocitrate dehydrogenase, aconitate hydratase (Japanese Patent Laid-open No. 63-214189) and so forth.

However, any L-amino acid biosynthesis enzymes and genes coding for them derived from thermophilic coryneform bacteria have not been reported.

Disclosure of the Invention

An object of the present invention is to provide genes coding for enzymes derived from *Corynebacterium thermoaminogenes*, preferably enzymes that function at a temperature higher than those of *Corynebacterium glutamicum*.

The inventors of the present invention extensively studied in order to achieve the aforementioned object. As a result, they successfully isolated genes coding for enzymes of the amino acid biosynthetic pathway of *Corynebacterium thermoaminogenes*, or genes coding for proteins involved in the uptake of amino acids into cells, and thus achieved the present invention.

That is, the present invention provides the followings.

(1) A protein having the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence of SEQ ID NO: 2 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has isocitrate lyase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 5 minutes.

(2) A protein having the amino acid sequence of SEQ ID NO: 4 or the amino acid sequence of SEQ ID NO: 4 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which is involved in acyl Co-A carboxylase activity derived from *Corynebacterium thermoaminogenes*.

(3) A protein having the amino acid sequence of SEQ ID NO: 6 or the amino acid sequence of SEQ ID NO: 6 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has DtsR activity derived from *Corynebacterium thermoaminogenes*.

(4) A protein having the amino acid sequence of SEQ ID NO: 8 or the amino acid sequence of SEQ ID NO: 8 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has DtsR activity derived from *Corynebacterium thermoaminogenes*.

(5) A protein having the amino acid sequence of SEQ ID NO: 10 or the amino acid sequence of SEQ ID NO: 10 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows phosphofructokinase activity at 60°C in an equivalent or higher degree compared with the activity at 30°C.

(6) A protein having the amino acid sequence of SEQ ID NO: 94 or the amino acid sequence of SEQ ID NO: 94 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has activity for imparting sucrose assimilating ability to *Corynebacterium thermoaminogenes*.

(7) A protein having any one of the amino acid sequences of SEQ ID NOS: 17-20 or the amino acid sequence of any one of SEQ ID NOS: 17-20 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has a function involved in glutamic acid uptake and derived from *Corynebacterium thermoaminogenes*.

(8) A protein having the amino acid sequence of SEQ ID NO: 22 or the amino acid sequence of SEQ ID NO: 22 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has pyruvate dehydrogenase activity derived from *Corynebacterium thermoaminogenes*.

(9) A protein having the amino acid sequence of SEQ ID

NO: 24 or the amino acid sequence of SEQ ID NO: 24 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has pyruvate carboxylase activity derived from *Corynebacterium thermoaminogenes*.

(10) A protein having the amino acid sequence of SEQ ID NO: 26 or the amino acid sequence of SEQ ID NO: 26 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has phosphoenolpyruvate carboxylase activity and shows 50% or more of residual activity after a heat treatment at 45°C for 5 minutes.

(11) A protein having the amino acid sequence of SEQ ID NO: 28 or the amino acid sequence of SEQ ID NO: 28 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has aconitase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 3 minutes.

(12) A protein having the amino acid sequence of SEQ ID NO: 30 or the amino acid sequence of SEQ ID NO: 30 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has isocitrate dehydrogenase activity and shows 50% or more of residual activity after a heat treatment at 45°C for 10 minutes.

(13) A protein having the amino acid sequence of SEQ ID NO: 32 or the amino acid sequence of SEQ ID NO: 32

including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has dihydrolipoamide dehydrogenase activity derived from *Corynebacterium thermoaminogenes*.

(14) A protein having the amino acid sequence of SEQ ID NO: 34 or the amino acid sequence of SEQ ID NO: 34 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has 2-oxoglutarate dehydrogenase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 10 minutes.

(15) A protein having the amino acid sequence of SEQ ID NO: 80 in Sequence Listing or the amino acid sequence of SEQ ID NO: 80 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows glutamate dehydrogenase activity at 42°C in an equivalent or higher degree compared with the activity at 37°C.

(16) A protein having the amino acid sequence of SEQ ID NO: 90 in Sequence Listing or the amino acid sequence of SEQ ID NO: 90 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.

(17) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence

of SEQ ID NO: 2 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having isocitrate lyase activity.

(18) The DNA according to (17), which is a DNA defined in the following (a1) or (b1):

(a1) a DNA which comprises the nucleotide sequence of SEQ ID NO: 1 in Sequence Listing,

(b1) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 1 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having isocitrate lyase activity.

(19) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 4 or the amino acid sequence of SEQ ID NO: 4 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and involved in acyl Co-A carboxylase activity.

(20) The DNA according to (19), which is a DNA defined in the following (a2) or (b2):

(a2) a DNA which comprises the nucleotide sequence of SEQ ID NO: 3 in Sequence Listing,

(b2) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 3 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein involved in acyl Co-A carboxylase activity.

(21) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 6 or the amino acid sequence of SEQ ID NO: 6 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having DtsR activity.

(22) The DNA according to (21), which is a DNA defined in the following (a3) or (b3):

(a3) a DNA which comprises the nucleotide sequence of SEQ ID NO: 5 in Sequence Listing,

(b3) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 5 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having DtsR activity.

(23) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 8 or the amino acid sequence of SEQ ID NO: 8 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having DtsR activity.

(24) The DNA according to (23), which is a DNA defined in the following (a4) or (b4):

(a4) a DNA which comprises the nucleotide sequence of SEQ ID NO: 7 in Sequence Listing,

(b4) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 7 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein

having DtsR activity.

(25) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 10 or the amino acid sequence of SEQ ID NO: 10 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having phosphofructokinase activity.

(26) The DNA according to (25), which is a DNA defined in the following (a5) or (b5):

(a5) a DNA which comprises the nucleotide sequence of SEQ ID NO: 9 in Sequence Listing,

(b5) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 9 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having phosphofructokinase activity.

(27) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 93 or the amino acid sequence of SEQ ID NO: 93 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having invertase activity.

(28) The DNA according to (27), which is a DNA defined in the following (a6) or (b6):

(a6) a DNA which comprises the nucleotide sequence of SEQ ID NO: 93 in Sequence Listing,

(b6) a DNA which is hybridizable with the

nucleotide sequence of SEQ ID NO: 93 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having invertase activity.

(29) A DNA which codes for a protein having any one of the amino acid sequences of SEQ ID NOS: 17-20 or the amino acid sequence of any one of SEQ ID NOS: 17-20 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having a function involved in glutamic acid uptake.

(30) The DNA according to (29), which is a DNA defined in the following (a7) or (b7):

(a7) a DNA which comprises the nucleotide sequence of SEQ ID NO: 16 in Sequence Listing,

(b7) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 16 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having a function involved in glutamic acid uptake.

(31) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 22 or the amino acid sequence of SEQ ID NO: 22 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having pyruvate dehydrogenase activity.

(32) The DNA according to (31), which is a DNA defined in the following (a8) or (b8):

(a8) a DNA which comprises the nucleotide sequence of SEQ ID NO: 21 in Sequence Listing,

(b8) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 21 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having pyruvate dehydrogenase activity.

(33) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 24 or the amino acid sequence of SEQ ID NO: 24 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having pyruvate carboxylase activity.

(34) A DNA according to (33), which is a DNA defined in the following (a9) or (b9):

(a9) a DNA which comprises the nucleotide sequence of SEQ ID NO: 23 in Sequence Listing,

(b9) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 23 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having pyruvate carboxylase activity.

(35) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 26 or the amino acid sequence of SEQ ID NO: 26 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having

phosphoenolpyruvate carboxylase activity.

(36) The DNA according to (35), which is a DNA defined in the following (a10) or (b10):

(a10) a DNA which comprises the nucleotide sequence of SEQ ID NO: 25 in Sequence Listing,

(b10) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 25 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having phosphoenolpyruvate carboxylase activity.

(37) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 28 or the amino acid sequence of SEQ ID NO: 28 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having aconitase activity.

(38) The DNA according to (37), which is a DNA defined in the following (a11) or (b11):

(a11) a DNA which comprises the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing,

(b11) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having aconitase activity.

(39) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 30 or the amino acid

sequence of SEQ ID NO: 30 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having isocitrate dehydrogenase activity.

(40) The DNA according to (39), which is a DNA defined in the following (a12) or (b12):

(a12) a DNA which comprises the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing,

(b12) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having isocitrate dehydrogenase activity.

(41) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 32 or the amino acid sequence of SEQ ID NO: 32 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having dihydrolipoamide dehydrogenase activity.

(42) The DNA according to (41), which is a DNA defined in the following (a13) or (b13):

(a13) a DNA which comprises the nucleotide sequence of SEQ ID NO: 31 in Sequence Listing,

(b13) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 31 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein

having dihydrolipoamide dehydrogenase activity.

(43) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 34 or the amino acid sequence of SEQ ID NO: 34 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having 2-oxoglutarate dehydrogenase activity.

(44) The DNA according to (43), which is a DNA defined in the following (a14) or (b14):

(a14) a DNA which comprises the nucleotide sequence of SEQ ID NO: 33 in Sequence Listing,

(b14) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 33 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having 2-oxoglutarate dehydrogenase activity.

(45) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 80 in Sequence Listing or the amino acid sequence of SEQ ID NO: 80 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and showing glutamate dehydrogenase activity at 42°C in an equivalent or higher degree compared with the activity at 37°C.

(46) The DNA according to (45), which is a DNA defined in the following (a15) or (b15):

(a15) a DNA which comprises the nucleotide

sequence of SEQ ID NO: 79 in Sequence Listing,

(b15) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 79 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein showing glutamate dehydrogenase activity at 42°C in an equivalent or higher degree compared with the activity at 37°C.

(47) A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 90 in Sequence Listing or the amino acid sequence of SEQ ID NO: 90 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and showing citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.

(48) The DNA according to (47), which is a DNA defined in the following (a16) or (b16):

(a16) a DNA which comprises the nucleotide sequence of SEQ ID NO: 89 in Sequence Listing,

(b16) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 89 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein showing citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.

(49) A method for producing L-amino acid, which

comprises culturing a microorganism introduced with a DNA according to any one of (17) to (48) in a medium to produce and accumulate L-amino acid in the medium, and collecting the L-amino acid from the medium.

The term "DNA of the present invention" is used hereinafter for referring to either one or all of the aforementioned DNAs.

Hereafter, the present invention will be explained in detail.

The nucleotide sequences of the DNA of the present invention, names of the genes, and the proteins encoded by the DNA of the present invention are shown in Table 1.

Table 1

Nucleotide sequence	Name of gene	Encoded protein (abbreviation)
SEQ ID NO: 1	*aceA*	Isocitrate lyase (ICL)
SEQ ID NO: 3	*accBC*	acyl Co-A carboxylase BC subunit
SEQ ID NO: 5	*dtsR1*	DTSR1 protein
SEQ ID NO: 7	*dtsR2*	DTSR2 protein
SEQ ID NO: 9	*pfk*	Phosphofructokinase
SEQ ID NOS: 11, 13, 15, 93	*scrB*	Invertase
SEQ ID NO: 16	*gluABCD*	glutamic acid uptake system
SEQ ID NO: 21	*pdhA*	pyruvate dehydrogenase
SEQ ID NO: 23	*pc*	pyruvate carboxylase
SEQ ID NO: 25	*ppc*	phosphoenolpyruvate carboxylase
SEQ ID NO: 27	*acn*	aconitase
SEQ ID NO: 29	*icd*	isocitrate dehydrogenase
SEQ ID NO: 31	*lpd*	dihydrolipoamide dehydrogenase
SEQ ID NO: 33	*odhA*	2-oxoglutarate dehydrogenase
SEQ ID NO: 79	*gdh*	glutamate dehydrogenase
SEQ ID NO: 89	*gltA*	citrate synthase

The open reading frames (ORFs) of SEQ ID NOS: 3, 23, 25, 31 and 33 and the fourth ORF of SEQ ID NO: 16 all start from GTG. Although the amino acids encoded by these GTG are indicated as valine in Sequence Listing, they may be methionine.

The sequence of SEQ ID NO: 16 contains four ORFs, which correspond to *gluA*, *gluB*, *gluC* and *gluD* in this order from the 5' end side.

The aforementioned DNA sequences were isolated from chromosomal DNA of the *Corynebacterium thermoaminogenes* AJ12310 strain (FERM BP-1542). However, the DNA sequences shown in SEQ ID NOS: 11 and 13 were isolated from *Corynebacterium thermoaminogenes* AJ12340 strain (FERM BP-1539) and AJ12309 strain (FERM BP-1541),

respectively, which had invertase activity and sucrose assimilating property, because the AJ12310 strain did not have invertase activity and sucrose assimilating property, and the *scrB* gene isolated from the strain had not any open reading frame.

The *Corynebacterium thermoaminogenes* AJ12310 strain (also referred to as YS-314 strain) and AJ12309 strain (also referred to as YS-155 strain) were deposited at the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Ministry of International Trade and Industry (postal code: 305-8566, 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan) on March 13, 1987 and given deposition numbers of FERM P-9246 and FERM P-9245, respectively. Then, they were transferred to international depositions under the provisions of the Budapest Treaty on October 27, 1987, and given deposition numbers of FERM BP-1542 and FERM BP-1541, respectively.

The AJ12340 strain (also referred to as YS-40 strain) was deposited at the National Institute of Bioscience and Human-Technology, Agency of Industrial Science and Technology, Ministry of International Trade and Industry (postal code: 305-8566, 1-3, Higashi 1-chome, Tsukuba-shi, Ibaraki-ken, Japan) on March 10, 1987 and given a deposition number of FERM P-9277. Then, it was transferred to an international deposition under

the provisions of the Budapest Treaty on October 27, 1987, and given a deposition number of FERM BP-1539.

The nucleotide sequences shown in SEQ ID NOS: 11, 13 and 15 are partial sequences of *scrB*, and the sequences of SEQ ID NOS: 11 and 13 code for partial amino acid sequences of invertase shown in SEQ ID NOS: 12 and 14.

A DNA sequence containing a partial fragment of a target gene can be obtained by comparing already reported nucleotide sequences for the target gene of various microorganisms such as *Brevibacterium lactofermentum* to select a region containing a well-conserved nucleotide sequence, and carrying out PCR using primers designed based on the nucleotide sequence of the region and chromosomal DNA of *Corynebacterium thermoaminogenes* as a template. Further, by performing hybridization using the obtained DNA fragment or a probe prepared based on the sequence of the fragment to screen a chromosomal DNA library of *Corynebacterium thermoaminogenes*, a DNA fragment containing the gene in its full length can be obtained. A DNA fragment containing the gene in its full length can also be obtained by performing genome walking using the obtained partial fragment of the gene. The genome walking can be carried out by using a commercially available kit, for example, TaKaRa LA PCR in vitro Cloning Kit (produced by Takara Shuzo).

For example, a partial sequence of DNA coding for glutamate dehydrogenase (henceforth the DNA is also referred to as "*gdh*", and the enzyme is also referred to as "GDH") can be obtained from chromosomal DNA of *Corynebacterium thermoaminogenes* such as the *Corynebacterium thermoaminogenes* AJ12310 strain by PCR (polymerase chain reaction) using the chromosomal DNA as a template and primers having the nucleotide sequences shown in SEQ ID NOS: 77 and 78 of Sequence Listing. Further, by performing genome walking using the obtained partial fragment, the whole *gdh* gene can be obtained.

Further, a partial sequence of DNA coding for citrate synthase (henceforth the DNA is also referred to as "*gltA*", and the enzyme is also referred to as "CS") can be obtained from chromosomal DNA of *Corynebacterium thermoaminogenes* such as the *Corynebacterium thermoaminogenes* AJ12310 strain by PCR (polymerase chain reaction) using the chromosomal DNA as a template and primers having the nucleotide sequences shown in SEQ ID NOS: 83 and 84 of Sequence Listing. Further, by performing genome walking using the obtained partial fragment, the whole *gltA* gene can be obtained.

The nucleotide sequences of the aforementioned primers were designed based on a nucleotide sequence in a region containing a well-conserved nucleotide sequence among the already reported *gdh* genes or *gltA* genes of various microorganisms, which region was found by

comparison of the genes.

As for DNA sequences coding for the other enzymes, partial fragments coding for those enzymes can be similarly obtained by using the primers mentioned in Table 1, and the genes in full length can be obtained by using the obtained partial fragments.

While the DNA of the present invention was obtained as described above, it can also be obtained from a chromosomal DNA library of *Corynebacterium thermoaminogenes* by hybridization using an oligonucleotide prepared based on the nucleotide sequences of the DNA of the present invention as a probe.

Methods for preparation of chromosomal DNA, construction of chromosomal DNA library, hybridization, PCR, preparation of plasmid DNA, digestion and ligation of DNA, transformation and so forth are described in Sambrook, J., Fritsch, E.F., Maniatis, T., Molecular Cloning, Cold Spring Harbor Laboratory Press, 1.21 (1989). Further, genome walking can be performed by using a commercially available kit, for example, TaKaRa LA PCR in vitro Cloning Kit (produced by Takara Shuzo).

Specific methods for obtaining the DNA of the present invention will be explained hereafter.

First, chromosomal DNA of *Corynebacterium thermoaminogenes* is digested with a suitable restriction enzyme, for example, *Sau*3AI, and fractionated by agarose gel electrophoresis to obtain a DNA fragment of about 4

to 6 kb. The obtained DNA fragment is inserted into a cloning vector such as pHSG399, and *Escherichia coli* is transformed with the obtained recombinant plasmid to produce a plasmid library of the chromosomal DNA.

Separately, primers are produced for use in selecting a clone containing a target gene from a plasmid library by PCR. These primers are designed based on conserved amino acid regions from various microorganisms corresponding to the gene of interest. In the design of primers, a plurality of primer sets are designed considering the codon usage of coryneform bacteria.

Then, in order to investigate propriety of the produced primers, PCR is performed by using these primers and chromosomal DNA of *Corynebacterium thermoaminogenes* as a template. Further, PCR is performed by using primers from which an amplification fragment has been obtained as primers for screening and a recombinant plasmid prepared from the plasmid library as a template to select a clone containing the target DNA fragment. This operation can be quickly carried out by performing the PCR for every batch including several tens of transformant strains as primary screening and performing colony PCR for the batch with which an amplification fragment was obtained as secondary screening. The fragment lengths of the amplified genes

are shown in Tables 2 to 7.

If a transformant selected as described above contains a target gene is confirmed by preparing a recombinant DNA from the transformant selected as described above, determining the nucleotide sequence of the inserted fragment by the dideoxy termination method, and comparing the nucleotide sequence with a known gene sequence.

When the obtained DNA fragment contains a part of the target gene, the deleted part is obtained by genome walking.

The DNA of the present invention may code for a protein including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, so long as the encoded protein has its original function. The number meant by the term "several" may vary depending on positions in the three-dimensional structure of protein or kinds of amino acid residues. However, in general, such a protein preferably shows homology of 30 to 40% or more, more preferably 55 to 65% or more, with respect to a corresponding whole amino acid sequence of the protein. More specifically, the term "several" means a number of 2 to several hundreds, preferably 2 to several tens, more preferably 2 to 10.

Nucleotide and amino acid sequence were analyzed by, for exmaple, the method developed by Lipman and

Peason (Science, 227, 1435-1441, 1985) by using commercially available softoware such as Genetyx-Mac computer program (Software Development Co., Tokyo, Japan).

GDH may be one showing homology of 40 to 80% or more, preferably 80 to 90% or more, for the total amino acid sequence constituting GDH, and showing GDH activity at 42°C equivalent to or higher than the activity at 37°C. In this case, the term "several" means a number of 2 to 30, preferably 2 to 50, more preferably 2 to 10.

CS may be one showing homology of 40 to 80% or more, preferably 80 to 90% or more, for the total amino acid sequence constituting CS, and showing CS activity at 37°C equivalent to or higher than the activity at 23°C. In this case, the term "several" means a number of 2 to 300, preferably 2 to 50, more preferably 2 to 10.

A DNA, which codes for the substantially same protein as the original protein as described above, can be obtained by, for example, modifying the nucleotide sequence, for example, by means of the site-directed mutagenesis so that one or more amino acid residues at a specific site should involve substitution, deletion, insertion, addition or inversion. A DNA modified as described above may also be obtained by a conventionally known mutation treatment. The mutation treatment includes a method for treating DNA coding for a target gene in vitro, for example, with hydroxylamine, and a

method for treating a microorganism, for example, a bacterium belonging to the genus *Escherichia*, harboring DNA coding for the target gene with ultraviolet irradiation or a mutating agent usually used for the mutation treatment such as N-methyl-N'-nitro-N-nitrosoguanidine (NTG) and nitrous acid.

The substitution, deletion, insertion, addition, or inversion of nucleotides as described above also includes mutant or variant that naturally occurs due to the difference of strains of *Corynebacterium thermoaminogenes* or the like.

A DNA coding for substantially the same protein as the original protein can be obtained by expressing DNA having a mutation in an appropriate cell, and investigating activity or function of the expressed product protein. The DNA coding for substantially the same protein as the original protein can also be obtained by, for example, isolating a DNA which is hybridizable with a DNA having each of the nucleotide sequences of the sequences of which sequence numbers are mentioned in Table 1 or a coding region thereof, or a probe designed based on the nucleotide sequence under a stringent condition, and which codes for a protein having the activity originally possessed by the protein, from DNA coding for a protein having a mutation or from a cell harboring it. The activity preferably means each enzymatic activity at 42°C for GDH or 37°C for CS.

The aforementioned probe can be prepared from a DNA having any one of the nucleotide sequences of which sequence numbers are shown in Table 1 or a DNA having any one of the nucleotide sequences by PCR using suitable primers.

The "stringent condition" referred to herein is a condition under which so-called specific hybrid is formed, and non-specific hybrid is not formed. It is difficult to clearly express this condition by using any numerical value. However, for example, the stringent condition includes a condition under which DNAs having high homology, for example, DNAs having homology of not less than 50% are hybridized with each other, and DNAs having homology lower than the above are not hybridized with each other. Alternatively, the stringent condition is exemplified by a condition under which DNAs are hybridized with each other at a salt concentration corresponding to an ordinary condition of washing in Southern hybridization, *i.e.*, 60°C, 1 x SSC, 0.1% SDS, preferably 0.1 x SSC, 0.1% SDS.

The gene, which is hybridizable under the condition as described above, includes those having a stop codon generated in the gene, and those having no activity due to mutation of active site. However, such genes can be easily removed by ligating the genes with a commercially available activity expression vector, and measuring the activity or function.

A protein corresponding to each DNA of the present invention can be produced by expressing the DNA in a suitable host-vector system.

As the host used for the expression of a gene, there can be mentioned various prokaryotic cells including *Brevibacterium lactofermentum* (*Corynebacterium glutamicum*), coryneform bacteria such as *Corynebacterium thermoaminogenes*, *Escherichia coli*, *Bacillus subtilis* and so forth, and various eucaryocytic cells including *Saccharomyces cerevisiae*, animal cells and plant cells. Among these, prokaryotic cells, in particular, coryneform bacteria and *Escherichia coli* are preferred.

If the DNA of the present invention is ligated to a vector DNA autonomously replicable in cells of *Escherichia coli* and/or coryneform bacteria and so forth to form a recombinant DNA, and this recombinant DNA is introduced into an *Escherichia coli* cell, the subsequent procedure becomes easy. The vector autonomously replicable in *Escherichia coli* cells is preferably a plasmid vector autonomously replicable in the host cell, and examples thereof include pUC19, pUC18, pBR322, pHSG299, pHSG399, pHSG398, RSF1010 and so forth.

As the vector autonomously replicable in coryneform bacterium cells, there can be mentioned pAM330 (refer to Japanese Patent Laid-open No. 58-67699/1983), pHM1519 (refer to Japanese Patent Laid-open No. 58-77895/1983) and so forth. Moreover, if a DNA

fragment having an ability to make a plasmid autonomously replicable in coryneform bacteria is taken out from these vectors and inserted into the aforementioned vectors for *Escherichia coli*, they can be used as a so-called shuttle vector autonomously replicable in both of *Escherichia coli* and coryneform bacteria.

Examples of such a shuttle vector include those mentioned below. There are also indicated microorganisms that harbor each vector, and accession numbers thereof at international depositories are shown in the parentheses, respectively.

pAJ655 *Escherichia coli* AJ11882 (FERM BP-136)
Corynebacterium glutamicum SR8201 (ATCC39135)

pAJ1844 *Escherichia coli* AJ11883 (FERM BP-137)
Corynebacterium glutamicum SR8202 (ATCC39136)

pAJ611 *Escherichia coli* AJ11884 (FERM BP-138)

pAJ3148 *Corynebacterium glutamicum* SR8203 (ATCC39137)

pAJ440 *Bacillus subtilis* AJ11901 (FERM BP-140)

pHC4 *Escherichia coli* AJ12617 (FERM BP-3532)

In order to prepare a recombinant DNA by ligating the DNA of the present invention and a vector that functions in coryneform bacteria, the vector is digested with a restriction enzyme that provides an end corresponding to an end of the DNA of the present invention. The ligation is normally attained by using a

ligase such as T4 DNA ligase.

To introduce the recombinant DNA prepared as described above into a host such as coryneform bacteria, any known transformation methods that have hitherto been reported can be employed. For instance, employable are a method of treating recipient cells with calcium chloride so as to increase the permeability for DNA, which has been reported for *Escherichia coli* K-12 (Mandel, M. and Higa, A., *J. Mol. Biol.*, *53*, 159 (1970)), and a method of preparing competent cells from cells which are at the growth phase followed by introducing the DNA thereinto, which has been reported for *Bacillus subtilis* (Duncan, C.H., Wilson, G.A. and Young, F.E., *Gene*, *1*, 153 (1977)). In addition to these, also employable is a method of making DNA-recipient cells into protoplasts or spheroplasts, which can easily take up recombinant DNA, followed by introducing the recombinant DNA into the cells, which is known to be applicable to *Bacillus subtilis*, actinomycetes and yeasts (Chang, S. and Choen, S.N., *Molec. Gen. Genet.*, *168*, 111 (1979); Bibb, M.J., Ward, J.M. and Hopwood, O.A., *Nature*, *274*, 398 (1978); Hinnen, A., Hicks, J.B. and Fink, G.R., *Proc. Natl. Sci. USA*, *75*, 1929 (1978)). The transformation of coryneform bacteria can be effectively performed by the electric pulse method (refer to Japanese Patent Laid-open No. 2-207791).

As for the transformation of thermophilic

coryneform bacteria such as *Corynebacterium thermoaminogenes*, it can be efficiently performed by treating cells with an agent that changes the structure of cell walls of the host cells, and applying an electric pulse to a solution containing DNA and the cells of which structure of the cell walls have been changed. The aforementioned agent is an agent that can change the structure of cell walls so that the cells can uptake the DNA when an electric pulse is applied to a solution containing the cells treated with the agent and the DNA (henceforth also referred to as a "cell wall treatment agent"). Examples of such an agent include agents that inhibit normal synthesis of bacterial cell wall and agents that lyse bacterial cell walls. Specific examples thereof include lysozyme, penicillin G, glycine and so forth.

Those cell wall treatment agents may be used each alone, or two or more kinds of them may be used in combination. Among the aforementioned agents, lysozyme and penicillin G are preferred, and lysozyme is particularly preferred.

Furthermore, the transformation of *Corynebacterium thermoaminogenes* can also be performed by applying an electric pulse to a solution containing DNA and the host cells of which cell walls has been weakened by a physical method such as ultrasonication (*FEMS Microbiology Letters*, *151*, 135-138 (1987)).

In order to efficiently express a gene contained in the DNA of the present invention, a promoter that functions in the host cell such as lac, trp and P_L may be ligated upstream from the coding region of the gene. If a vector containing a promoter is used as the vector, ligation of each gene, vector and promoter can be attained by one step.

The proteins of the present invention, which can be produced as described above, can be purified as required from a cell extract or medium by using usual methods for purifying enzymes such as ion exchange chromatography, gel filtration chromatography, adsorption chromatography, salting out and solvent precipitation.

It is expected that the proteins of the present invention are excellent in thermal stability or exhibit higher activity at high temperatures compared with the corresponding proteins of *Corynebacterium glutamicum* and so forth. For example, GDH of *Brevibacterium lactofermentum* shows the highest GDH specific activity around 37°C, and the activity is markedly reduced around 42°C. However, GDH of the present invention shows at 42°C the GDH activity equivalent to or higher than the activity at 37°C. In a preferred embodiment, GDH of the present invention shows the highest specific activity around 42°C, and shows the activity even at 45°C.

The GDH activity can be measured by, for example,

adding the enzyme to 100 mM Tris-HCl (pH 8.0), 20 mM NH_4Cl, 10 mM sodium α-ketoglutarate, 0.25 mM NADPH, and determining change of absorbance at 340 nm (Molecular Microbiology 6, 317-326 (1992)).

Further, CS of *Brevibacterium lactofermentum* shows the highest CS specific activity around 23°C, and the activity is markedly reduced around 33°C. To the contrary, CS of the present invention shows at 37°C the CS activity equivalent to or higher than the activity at 23°C. In a preferred embodiment, CS of the present invention shows reaction temperature-dependently higher activity up to around 37°C, and shows, even at 40°C, about 40% of the activity with respect to the activity at 37°C.

The CS activity can be measured by, for example, the method described in Methods in Enzymol., 13, 3-11 (1969).

Further, other proteins of the present invention typically have the following characteristics. The isocitrate lyase has 30% or more of residual activity after a heat treatment at 50°C for 5 minutes. The phosphofructokinase has, at 60°C, the activity equivalent to or higher than the activity at 30°C. The phosphoenolpyruvate carboxylase has 50% or more of residual activity after a heat treatment at 45°C for 5 minutes. The aconitase has 30% or more of residual activity after a heat treatment at 50°C for 3 minutes.

The isocitrate dehydrogenase has 50% or more of residual activity after a heat treatment at 45°C for 10 minutes. The 2-oxoglutarate dehydrogenase has 30% or more of residual activity after a heat treatment at 50°C for 10 minutes.

The proteins of the present invention can also be obtained from cell extracts of *Corynebacterium thermoaminogenes* such as the *Corynebacterium thermoaminogenes* AJ12310 strain by using each activity as an index and usual purification methods for purifying enzymes such as ion exchange chromatography, gel filtration chromatography, adsorption chromatography, salting out and solvent precipitation.

Among the DNA of the present invention, *pfk*, *pdhA*, *pc*, *ppc*, *acn*, *icd*, *gdh* and *gltA* (names of the enzymes encoded by these are shown in Table 1) can be introduced into L-amino acid production bacteria such as coryneform bacteria to enhance their L-amino acid producing ability. It is also expected that coryneform bacteria introduced with the DNA of the present invention become possible to produce L-amino acid at a temperature higher than usual. The L-amino acid includes L-glutamic acid, L-aspartic acid, L-lysine, L-arginine, L-proline, L-glutamine and so forth.

For example, it is expected that L-glutamic acid production bacteria such as coryneform bacteria

introduced with the *gdh* gene or *gltA* gene come to be able to produce L-glutamic acid at a temperature higher than usual. Further, although CS of *Brevibacterium lactofermentum* may not fully function at a usual culture temperature, for example, 31.5°C, the activity can be enhanced by introducing the *gltA* gene of the present invention.

Further, *dtsR1* and *dtsR2* are genes that code for proteins imparting resistance to surfactant to coryneform bacteria (DTSR protein), and coryneform L-glutamic acid producing bacteria of which these genes are disrupted produce a marked amount of L-glutamic acid even under a condition where biotin is present in such an amount that a wild strain becomes to be substantially unable to produce L-glutamic acid. Further, if *dtsR1* and *dtsR2* genes of coryneform L-glutamic acid producing bacteria having L-lysine producing ability are amplified, the bacteria are imparted with an ability to produce a marked amount of L-lysine (WO95/23224, Japanese Patent Laid-open (Kokai) No. 10-234371/1998).

The *scrB* gene can be used for improvement of coryneform bacteria for use in the production of L-amino acids by using coryneform bacteria in a medium containing sucrose.

By deleting *aceA*, *accBC*, *lpd* or *odhA* of L-glutamic acid producing coryneform bacteria and so forth, their

L-glutamic acid productivity can be enhanced. Further, *gluABCD* is a gene cluster of the L-glutamic acid uptake system, and by deleting one to four of *gluA*, *gluB*, *gluC* and *gluD* in coryneform L-glutamic acid producing bacteria, the amount of L-glutamic acid accumulated in the medium can be increased. *aceA*, *accBC*, *lpd*, *odhA* and *gluABCD* of the present invention can be used for disruption of these genes on chromosome.

The medium used for producing L-amino acids by utilizing a microorganism introduced with the DNA of the present invention may be a usual medium that contains a carbon source, a nitrogen source, inorganic ions and other organic trace nutrients as required. As the carbon source, there can be used hydrocarbons such as glucose, lactose, galactose, fructose, sucrose, blackstrap molasses and starch hydrolysate; alcohols such as ethanol and inositol; or organic acids such as acetic acid, fumaric acid, citric acid and succinic acid.

As the nitrogen source, there can be used inorganic ammonium salts such as ammonium sulfate, ammonium nitrate, ammonium chloride, ammonium phosphate and ammonium acetate, ammonia, organic nitrogen such as peptone, meat extract, yeast extract, corn steep liquor and soybean hydrolysate, ammonia gas, aqueous ammonia and so forth.

As the inorganic ions (or sources thereof), added is a small amount of potassium phosphate, magnesium

sulfate, iron ions, manganese ions and so forth. As for the organic trace nutrients, it is desirable to add required substances such as vitamin B_1, yeast extract and so forth in a suitable amount as required.

The culture is preferably performed under an aerobic condition attained by shaking, stirring for aeration or the like for 16 to 72 hours. The culture temperature is controlled to be at 30°C to 47°C, and pH is controlled to be 5 to 9 during the culture. As for the culture temperature, the culture may be performed at a temperature suitable for culture of a microorganism not introduced with the DNA of the present invention or a temperature higher than that. For adjustment of pH, inorganic or organic acidic or alkaline substances, ammonia gas and so forth can be used.

Collection of L-amino acids from fermentation broth can be attained by a combination of known methods such as techniques utilizing ion exchange resin, precipitation, crystallization and so forth depending on the kind of the L-amino acids.

Brief Explanation of the Drawings

Fig. 1 shows variation with temperature in activity of glutamate dehydrogenases derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and the *Brevibacterium lactofermentum* 2256 strain.

Fig. 2 shows thermal stability of glutamate

dehydrogenases derived from the AJ12310 strain and the 2256 strain.

Fig. 3 shows variation with temperature in activity of citrate synthases derived from the AJ12310 strain and the 2256 strain.

Fig. 4 shows thermal stability of citrate synthases derived from the AJ12310 strain and the 2256 strain.

Fig. 5 shows variation with temperature in activity of isocitrate lyases derived from the AJ12310 strain and the 2256 strain.

Fig. 6 shows thermal stability of isocitrate lyases derived from the AJ12310 strain and the 2256 strain.

Fig. 7 shows variation with temperature in activity of phosphofructokinases derived from the AJ12310 strain and the 2256 strain.

Fig. 8 shows thermal stability of phosphofructokinases derived from the AJ12310 strain and the 2256 strain.

Fig. 9 shows variation with temperature in activity of phosphoenolpyruvate carboxylases derived from the AJ12310 strain and the 2256 strain.

Fig. 10 shows thermal stability of phosphoenolpyruvate carboxylases derived from the AJ12310 strain and the 2256 strain.

Fig. 11 shows variation with temperature in

activity of aconitases derived from the AJ12310 strain and the 2256 strain.

Fig. 12 shows thermal stability of aconitases derived from the AJ12310 strain and the 2256 strain.

Fig. 13 shows variation with temperature in activity of isocitrate dehydrogenases derived from the AJ12310 strain and the 2256 strain.

Fig. 14 shows thermal stability of isocitrate dehydrogenases derived from the AJ12310 strain and the 2256 strain.

Fig. 15 shows thermal stability of 2-oxoglutarate dehydrogenases derived from the AJ12310 strain and the 2256 strain.

Fig. 16 shows construction of plasmid pSCR155 carrying *scrB* gene.

Fig. 17 shows construction of plasmid pPDHA-2 carrying *pdhA* gene.

Fig. 18 shows L-glutamic acid productivity of a *pdhA* gene-amplified strain: (a) 37°C and (b) 44°C.

Fig. 19 shows is construction of a plasmid pICD-4 carrying *icd* gene.

Fig. 20 shows L-glutamic acid productivity of an *icd* gene-amplified strain: (a) 37°C and (b) 44°C.

Fig. 21 shows construction of plasmids pHSG299YGDH and pYGDH.

Fig. 22 shows construction of plasmids pHSG299YCS and pYCS.

Best Mode for Carrying out the Invention

Hereafter, the present invention will be further specifically explained with reference to the following examples.

Example 1

<1> Production of plasmid library of *Corynebacterium thermoaminogenes*

The *Corynebacterium thermoaminogenes* AJ12310 strain was cultured in CM2B liquid medium (1 g/dl of yeast extract (produced by Difco), 1 g/dl of polypeptone (produced by Nippon Seiyaku), 0.5 g/dl of NaCl, 10 μg/dl of biotin, pH 7.0 (adjusted with KOH)) at 37°C for 15 hours, and its chromosomal DNA was prepared from the 10 ml of the medium by using a chromosomal DNA extraction kit (Bacterial Genome DNA Purification Kit (produced by Advanced Genetic Technologies)). The obtained DNA was partially digested with a restriction enzyme *Sau*3AI, and subjected to 0.8% agarose gel electrophoresis to fractionate the DNA. Then, a band corresponding to a DNA fragment of about 4 to 6 kb was excised from the gel, and a DNA fragment of the objective size was obtained by using a DNA gel extraction kit (GIBCO BRL, Concert™ Rapid Gel Extraction System).

The plasmid pHSG399 (produced by Takara Shuzo) was fully digested with *Bam*HI, and its end was

dephosphorylated by using alkaline phosphatase (CIAP; produced by Takara Shuzo). This vector fragment and the aforementioned chromosomal DNA fragment were ligated by using a DNA ligation kit produced by Takara Shuzo, and *Escherichia coli* JM109 was the transformed with the obtained recombinant vector. Selection of transformants was performed on LB agar medium (containing 1.5 g/dl of agar) containing 30 μg/ml of chloramphenicol, 0.04 mg/ml of IPTG (isopropyl-β-D-thiogalactopyranoside) and 0.04 mg/ml of X-Gal (5-bromo-4-chloro-3-indolyl-β-D-galactoside) to obtain about 4000 white colonies.

<2> Design of primers for amplification of each gene

Primers for use in selection of a clone containing each target gene by PCR from the plasmid library obtained above were designed. The target genes were mentioned above.

The primers were designed based on a known gene sequence of coryneform bacteria, *i.e.*, its sequence of a region where conservation at the amino acid level was observed when compared with corresponding genes of other microorganisms. Considering the codon usage of coryneform bacteria, a plurality of primer sets were designed for each gene.

To examine propriety of the prepared primers, PCR was performed by using these primers and chromosomal DNA of the *Corynebacterium thermoaminogenes* AJ12310 strain

as a template to amplify each gene fragment. As a result, when the PCR was performed by using the primers shown in the upper rows of Tables 2 to 7 under the conditions indicated as "PCR conditions for obtaining partial fragment" in the tables, an amplified fragment was observed for all of the genes. The parenthesized numbers after the primer sequences indicate the sequence numbers in Sequence Listing. These primers were used as primers for screening mentioned below.

Table 2

Gene	*aceA*	*accBC*	*dtsR1*
5'→3'Primer	CCTCTACCCAGCGAACTCCG (35)	CATCCACCCCGGCTACGGCT (37)	ACGGCCCAGCCCTGACCGAC (39)
3'→5'Primer	CTGCCTTGAACTCACGGTTC (36)	CGGTGACTGGGTGTTCCACC (38)	AGCAGCGCCCATGACGGCGA (40)
PCR conditions for obtaining partial fragment and PCR conditions for screening	94°C, 5 min 98°C, 5 sec 66°C, 2 sec, 30 cycles Z-Taq	94°C, 5 min 98°C, 5 sec 66°C, 2 sec, 30 cycles Z-Taq	94°C, 5 min 98°C, 5 sec 66°C, 2 sec, 30 cycles Z-Taq
Conditions of colony PCR	94°C, 7 min 91°C, 30 sec 55°C, 1 sec 72°C, 2.5 min, 30 cycles Ex-Taq	94°C, 7 min 91°C, 30 sec 55°C, 1 sec 72°C, 2.5 min, 30 cycles Ex-Taq	94°C, 7 min 91°C, 30 sec 55°C, 1 sec 72°C, 2.5 min, 30 cycles Ex-Taq
Amplified fragment	824bp	673bp	805bp

Table 3

Gene	*dtsR2*	*pfk*	*scrB*
5'→3'Primer	ACGGCCCAGCCCTGACCGAC (41)	CGTCATCCGAGGAATCGTCC (43)	GGNCGHYTBAAYGAYCC (45)
3'→5'Primer	AGCAGCGCCCATGACGGCGA (42)	CGTGGCGGCCCATGACCTCC (44)	GGRCAYTCCCACATRTANCC (46)
PCR conditions for obtaining partial fragment and PCR conditions for screening	94°C, 5 min 98°C, 5 sec 66°C, 2 sec, 30 cycles Z-Taq	94°C, 5 min 98°C, 5 sec 66°C, 2 sec, 30 cycles Z-Taq	94°C, 5 min 98°C, 5 sec 50°C, 10 sec 72°C, 20 sec, 40 cycles Z-Taq
Conditions of colony PCR	94°C, 7 min 91°C, 30 sec 55°C, 1 sec 72°C, 2.5 min, 30 cycles Ex-Taq	94°C 7 min 91°C 30 sec 55°C 1 sec 72°C 2.5 min 30 cycles Ex-Taq	94°C, 7 min 91°C, 30 sec 55°C, 1 sec 72°C, 2.5 min, 30 cycles Ex-Taq
Amplified fragment	805bp	472bp	500bp

Table 4

Gene	*gluABCD*	*pdhA*
5'→3'Primer	CCATCCGGATCCGGCAAGTC (47)	ACTGTGTCCATGGGTCTTGGCCC (49)
3'→5'Primer	AATCCCATCTCGTGGGTAAC (48)	CGCTGGAATCCGAACATCGA (50)
PCR conditions for obtaining partial fragment	94°C, 5 min 98°C, 5 sec 50°C, 10 sec 72°C, 20 sec, 30 cycles Z-Taq	94°C, 5 min 98°C, 5 sec 50°C, 10 sec 72°C, 20 sec, 30 cycles Z-Taq
Amplified fragment	500bp	1200bp
Conditions for screening PCR and colony PCR	94°C, 5 min 94°C, 30 sec 50°C, 1 min 72°C, 2 min, 30 cycles EX-Taq	94°C, 5 min 94°C, 30 sec 50°C, 1 min 72°C, 2 min, 30 cycles EX-Taq

Table 5

Gene	*pc*	*ppc*
5'→3'Primer	GGCGCAACCTACGACGTTGCAATGCG (51)	GGTTCCTGGATTGGTGGAGA(53)
3'→5'Primer	TGGCCGCCTGGGATCTCGTG (52)	CCGCCATCCTTGTTGGAATC(54)
PCR conditions for obtaining partial fragment	94°C, 5 min 98°C, 5 sec 55°C, 80 sec 30 cycles Z-Taq	94°C 5 min 98°C 5 sec 50°C 5 sec 72°C 10 sec 30 cycles Z-Taq
Amplified fragment	781bp	1000bp
Conditions for screening PCR	94°C, 5 min 98°C, 5 sec 55°C, 80 sec 30 cycles Z-Taq	94°C, 5 min 98°C, 5 sec 50°C, 5 sec 72°C, 10 sec, 30 cycles Z-Taq
Conditions for colony PCR	94°C, 5 min, 1 cycles 98°C, 5 sec 55°C, 80 sec, 50 cycles Z-Taq	94°C, 5 min 98°C, 5 sec 50°C, 10 sec 72°C, 20 sec, 50 cycles Z-Taq

Table 6

Gene	*acn*	*icd*	*lpd*
5'→3'Primer	GTIGGIACIGAYTCSCATAC (55)	GACATTTCACTCGCTGGACG (57)	ATCATCGCAACCGGTTC (59)
3'→5'Primer	GCIGGAGAIATGTGRTCIGT (56)	CCGTACTCTTCAGCCTTCTG (58)	CGTCACCGATGGCGTAAAT (60)
PCR conditions for obtaining partial fragment	94°C, 1 min 96°C, 20 sec 45°C, 1 min 68°C, 2 min, 30 cycles EX-Taq	94°C, 5 min 98°C, 5 sec 55°C, 80 sec, 30 cycles Z-Taq	94°C, 5 min 98°C, 5 sec 50°C, 10 sec 72°C, 20 sec, 30 cycles Z-Taq
Amplified fragment	1500bp	1500bp	500bp
Conditions for screening PCR and colony PCR Screening PCR 5'→3'Primer 3'→5'Primer	Same as above	Same as above	94°C, 5 min 94°C, 30 sec 57°C, 1 min 72°C, 1 min, 30 cycles Ex-Taq TACGAGGAGCAGATCCTCAA (63) TTGACGCCGGTGTTCTCCAG (64)

Table 6 (Cont.)

Gene	*acn*	*icd*	*Lpd*
LA cloning (N') 3'→5'Primer	S1:GGTGAAGCTAAGTAGTTAGC 65) S2:AGCTACTAAACCTGCACC (66)	S1:CCGTACTCTTCAGCCTTCTG(67) S2:TCGTCCTTGTTCCACATC (68)	S1:ATCATCGCAACCGGTTC (69) S2:TACGAGGAGCAGATCCTCAA(70)
LA Cloning (C') 5'→3'Primer	S1:GCTAACTACTTAGCTTCACC(71) S2:GAACCAGGAACTATTGAACC(72)	S1:TCCGATGTCATCATCGAC (73) S2:ATGTGGAACAAGGACGAC (74)	
Restrictione enzyme	PstI(N') HindIII(C')	SalI(N') PstI(C')	HindIII
Conditions for LA cloning	N' 94°C, 1 min 94°C, 30 sec 57°C, 2 min 72°C, 2 min, 30 cycles LA-Taq C' 94°C, 1 min 94°C, 30 sec 57°C, 2 min 72°C, 2.5 min, 30 cycles LA-Taq	94°C, 1 min 94°C, 30 sec 57°C, 2 min 72°C, 2.5 min, 30 cycles LA-Taq	94°C, 1 min 94°C, 30 sec 57°C, 2 min 72°C, 1 min, 30 cycles LA-Taq

Table 7

Gene	*odhA*
5'→3'Primer 3'→5'Primer	ACACCGTGGTCGCCTCAACG (61) TGCTAACCCGTCCCACCTGG (62)
PCR conditions for obtaining partial fragment	94°C, 5 min 98°C, 5 sec 66°C, 2 sec, 30 cycles Z-Taq
Amplified fragment	1306bp
LA cloning (N') 5'→3'Primer	S1:GTACATATTGTCGTTAGAACGCGTAATACGACTCA(75) S2:CGTTAGAACGCGTAATACGACTCACTATAGGGAGA(76)
Restriction	XbaI
Conditions for LA cloning	First time 94°C, 30 sec 55°C, 2 min 72°C, 1 min 30 cycles LA-Taq Second time 94°C, 1 min 98°C, 20 sec 68°C, 15 min, 30 cycles 72°C 10 min LA-Taq

<3> Screening of plasmid library by PCR

A clone containing a target gene was selected from the plasmid library by PCR. Sixty colonies were picked up from each plasmid library, and replicated onto two LB agar medium plates. The 60 colonies of each plate were combined, inoculated to a test tube containing 4 ml of LB liquid medium and cultured for 15 hours. Then, a plasmid mixture was respectively obtained by using a plasmid DNA extraction kit produced by Promega. By using this plasmid mixture as a template and primers for screening prepared for each target gene, PCR was performed with the conditions shown as "conditions for screening PCR" in each table to select a clone from which a DNA fragment of the same size as that obtained by PCR using chromosomal DNA as a template had been amplified.

The nucleotide sequence of the amplified DNA fragment was determined by using a Big Dye dye terminator cycle sequencing kit produced by Perkin-Elmer, and investigating its homology to known gene information to determine if the target gene was obtained or not.

As for *lpd*, since any DNA fragment was not amplified with the primers produced in <2>, other primers for screening were prepared based on the determined nucleotide sequence.

<4> Selection of clone harboring target gene by colony

PCR

By using a plate that was an origin of a plasmid mixture for which amplification of the target gene fragment was confirmed, colony PCR was performed to select a clone containing the gene fragment. The colony PCR was performed with the conditions shown in Tables 2-7.

Plasmid DNA was collected from a selected transformant and the nucleotide sequence of the inserted DNA fragment was determined. When the full length of the target gene was not inserted in the inserted DNA fragment, and a upstream region, downstream region or the both were deleted, primers were prepared based on the determined nucleotide sequence, with which a gene fragment comprising the nucleotide sequence of the target gene in its full length was obtained by using TaKaRa LA PCR in vitro Cloning Kit (Takara Shuzo). Then, its nucleotide sequence was determined.

The outline of LA PCR cloning was as follows. Two kinds of primers each having one of the nucleotide sequences of two regions of the inserted DNA fragment were produced. Chromosomal DNA of *Corynebacterium thermoaminogenes* AJ12310 strain was digested with various restriction enzymes, and ligated to a cassette primer corresponding to each of the restriction enzymes. By using this as a template, PCR was performed with a primer (S1) corresponding to a position distant from the

deletion region and a cassette primer (C1) corresponding to a position outside the cassette primer among the prepared primers. Then, another PCR was performed with a primer (S2) corresponding to a position near the deletion region and a cassette primer (C2) corresponding to a position inside the cassette primer among the prepared primers. In this way, a DNA fragment containing the deleted region was obtained. By ligating the obtained DNA fragment with the already obtained DNA fragment, a DNA fragment containing the target gene in full length could be obtained. Since 5′ end of the cassette did not have a phosphate group, a nick was formed at the ligation site of the 3′ end of the DNA fragment and the 5′ end of the cassette. Therefore, the DNA synthesis from the primer C1 stopped at this ligation site in the first PCR, and thus non-specific amplification did not occur. Therefore, specific amplification could be attained.

The primers and the reaction conditions used for the LA PCR cloning are shown in Tables 2-7. In the tables, the primers mentioned with "(N′)" are primers used for the cloning of an upstream deleted portion, and the primers mentioned with "(C′)" are primers used for the cloning of a downstream deleted portion. PCR was performed twice according to the instruction attached to the LA PCR cloning kit. Among the primers mentioned in the tables, the primers (S1) used for the first reaction

are shown in the upper row, and the primers (S2) used for the second reaction are shown in the lower row.

The nucleotide sequences of the DNA fragments containing each gene obtained as described above were determined in the same manner as mentioned above. Those nucleotide sequences and amino acid sequences that can be encoded by those nucleotide sequences are shown in SEQ ID NOS: 1-34. The sequences shown with the sequence numbers are summarized in Explanation of Sequence Listing mentioned hereinafter.

As for *scrB*, any open reading frame was not found. Since the *Corynebacterium thermoaminogenes* AJ12310 strain did not have the invertase activity and did not have sucrose assimilating property, an *scrB* gene fragment was obtained in a similar manner from *Corynebacterium thermoaminogenes* AJ12340 and AJ12309 strains having the sucrose assimilating property. As a result, a DNA fragment having an open reading frame was obtained from the both strains.

Example 2: Acquisition of *gdh* and *gltA* gene

<1> Investigation of GDH activity of *Corynebacterium thermoaminogenes*

Cells of a wild strain of *Corynebacterium thermoaminogenes*, the AJ12310 strain, was grown on CM-2B agar medium (1 g/dl of yeast extract (produced by Difco), 1 g/dl of polypeptone (produced by Nippon Seiyaku), 0.5

g/dl of NaCl, 10 μg/dl of biotin, 1.5 g/dl of agar, adjusted to pH 7.0 with KOH). The cells were inoculated to a 500-ml volume flask containing 20 ml of a medium for flask having the following composition and cultured at 37°C for 17 hours (until the residual sugar reached about 1 g/dl).

Similarly, cells of the 2256 strain (ATCC13869) of *Brevibacterium lactofermentum* grown on CM-2B agar medium were cultured at 31.5°C for 17 hours.

[Medium for flask]

Glucose	3 g/dl
KH_2PO_4	0.1 g/dl
$MgSO_4 \cdot H_2O$	0.04 g/dl
$FeSO_4 \cdot 7H_2O$	1 mg/dl
$MnSO_4 \cdot 4H_2O$	1 mg/dl
Vitamin B_1-HCl	200 μg/L
Biotin	50 μg/L
$(NH_4)_2SO_4$	1.5 g/dl
Soybean protein hydrolysis solution (Memeno (T-N))	48 mg/dl
$CaCO_3$ (Official regent)	5 g/dl (separately sterilized)
pH 8.0 (adjusted with KOH)	

About 1 ml of the above culture medium was centrifuged at 1000 rpm for 1 minute to remove $CaCO_3$, and the cells were washed twice with 200 mM K-phosphate

buffer (pH 6.9) and suspended in 300 μl of the same buffer. The obtained cell suspension was sonicated for 5 minutes to disrupt the cells, centrifuged at 1000 rpm for 30 minutes to obtain a crude enzyme solution as the supernatant.

The optimum reaction temperature and the thermal stability of GDH activity were investigated using the aforementioned crude enzyme solution. The measurement of GDH activity was performed by adding the crude enzyme solution to a reaction mixture (100 mM Tris-HCl (pH 8.0), 20 mM NH_4Cl, 10 mM sodium α-ketoglutarate, 0.25 mM NADPH) and measuring change of absorbance at 340 nm. The protein concentration of the crude enzyme solution was quantified by the Bradford method (Bio-Rad Protein Assay Kit was used) using bovine serum albumin as the standard through measurement of absorbance at 595 nm. The absorbance was measured by using HITACHI U-2000 (produced by Hitachi).

The GDH activity measured at various reaction temperatures is shown in Fig. 1. While the ATCC13869 strain showed the highest specific activity of GDH around 37°C and the activity markedly decreased around 42°C, the AJ12310 strain showed the highest specific activity around 42°C and it showed the activity even at 45°C.

Then, the thermal stability of GDH was investigated. The crude enzyme solution was left at

65°C for 0 to 30 minutes before the reaction, and then the enzyme activity was measured at 30°C. The results are shown in Fig. 2. As clearly seen from the results, while GDH of the ATCC13869 strain was inactivated by the heat treatment for 5 minutes, GDH of the AJ12310 strain maintained the activity even after the heat treatment for 30 minutes. In addition, the crude enzyme solution of the AJ12310 strain showed substantially no change in the GDH activity even after the heat treatment at 65°C for 90 minutes (data are not shown).

<2> Examination of CS activity of *Corynebacterium thermoaminogenes*

The optimum reaction temperature and thermal stability of CS were investigated by using crude enzyme solutions prepared from the cells of the *Corynebacterium thermoaminogenes* AJ12310 strain and the *Brevibacterium lactofermentum* ATCC13869 strain in the same manner as in Example 1. The measurement of CS activity was performed by adding each crude enzyme solution to a reaction mixture (100 mM Tris-HCl (pH 8.0), 0.1 mM DTNB (5,5'-dithiobis-(2-nitrobenzoic acid)), 200 mM sodium L-glutamate, 0.3 mM acetyl CoA), and measuring change of the absorbance at 412 nm.

The CS activity measured at various reaction temperatures is shown in Fig. 3. The ATCC13869 strain showed the highest specific activity of CS around 23°C

and the activity markedly decreased around 33°C. However, the AJ12310 strain showed high specific activity in a reaction temperature-dependent manner up to around 37°C and it showed the activity even at 40°C in a degree corresponding to about 40% of the activity at 37°C.

Then, thermal stability of CS was investigated. The crude enzyme solution was left at 33-55°C for 5 minutes before the reaction, and then the enzyme activity was measured at 30°C. The results are shown in Fig. 4. Whereas CS of the ATCC13869 strain was inactivated by the heat treatment at 35-40°C, CS of the AJ12310 strain maintained about 40% of the activity even after the heat treatment at 50°C.

<3> Acquisition of *gdh* gene of *Corynebacterium thermoaminogenes*

The already reported nucleotide sequences of *gdh* gene of various microorganisms were compared. A region in which nucleotide sequences were well conserved was selected, and primers having the nucleotide sequences shown in SEQ ID NOS: 77 and 78 were prepared based on the nucleotide sequence of the region.

PCR was performed by using chromosomal DNA prepared from the *Corynebacterium thermoaminogenes* AJ12310 strain using Bacterial Genome DNA Purification Kit (produced by Advanced Genetic Technologies) as a

template and the aforementioned primers. Based on the obtained DNA fragment, genome walking was performed by using TaKaRa LA PCR in vitro Cloning Kit (produced by Takara Shuzo) to obtain the whole *gdh* gene, of which whole nucleotide sequence was determined. The result is shown in SEQ ID NO: 79. Further, the amino acid sequence deduced from this nucleotide sequence is shown in SEQ ID NO: 80.

The *gdh* gene of the *Brevibacterium lactofermentum* ATCC13869 strain was obtained in a similar manner, and its nucleotide sequence was determined. The result is shown in SEQ ID NO: 81. The amino acid sequence encoded by this nucleotide sequence is shown in SEQ ID NO: 82.

Homology was investigated for the nucleotide sequences of the *gdh* gene and the amino acid sequences of GDH of the *Corynebacterium thermoaminogenes* AJ12310 strain and the *Brevibacterium lactofermentum* ATCC13869 strain determined as described above, and the known *gdh* gene and amino acid sequence of GDH of the *Corynebacterium glutamicum* (*C. glutamicum*) ATCC13032 strain (Molecular Microbiology 6, 317-326 (1992)). The results are shown in Table 8 (for nucleotide sequences) and Table 9 (for amino acid sequences).

Table 8: Homology of nucleotide sequences of various *gdh* genes

	ATCC13869	ATCC13032	AJ12310
ATCC13869	-	94.5%	82.4%
ATCC13032	-	-	78.1%
AJ12310	-	-	-

Table 9: Homology of amino acid sequences of various GDH

	ATCC13869	ATCC13032	AJ12310
ATCC13869	-	90.8%	91.7%
ATCC13032	-	-	83.4%
AJ12310	-	-	-

<4> Acquisition of *gltA* gene of *Corynebacterium thermoaminogenes*

The already reported nucleotide sequences of *gltA* gene of various microorganisms were compared. A region in which nucleotide sequences were well conserved was selected, and primers having the nucleotide sequences shown in SEQ ID NOS: 83 and 84 were prepared based on the nucleotide sequence of the region.

PCR was performed by using chromosomal DNA prepared from the *Corynebacterium thermoaminogenes* AJ12310 strain (FERM BP-1542) using Bacterial Genome DNA Purification Kit (produced by Advanced Genetic Technologies) as a template and the aforementioned primers 7 and 8, and the nucleotide sequence of the amplified nucleotide sequence of about 0.9 kb was determined.

On the basis of the obtained nucleotide sequence of *gltA* gene of *Corynebacterium glutamicum* (Microbiol., 140, 1817-1828 (1994)), the primers of SEQ ID NOS: 85, 86, 87 and 88 were prepared. PCR was performed in a manner similar to the above by using chromosomal DNA of AJ12310 as a template and the primers of SEQ ID NOS: 85, 86, 87 and 88, and the nucleotide sequence of the amplified DNA fragment was specified to determine the whole nucleotide sequence of the *gltA* gene. The result is shown in SEQ ID NO: 89. Further, an amino acid sequence expected from this nucleotide sequence is shown in SEQ ID NO: 90.

The *gltA* gene of the *Brevibacterium lactofermentum* 2256 strain was obtained in a similar manner, and its nucleotide sequence was determined. The result is shown in SEQ ID NO: 91. The amino acid sequence encoded by this nucleotide sequence is shown in SEQ ID NO: 92.

Homology was investigated for the nucleotide sequences of the *gltA* gene and the amino acid sequences of CS of the *Corynebacterium thermoaminogenes* AJ12310 strain and the *Brevibacterium lactofermentum* ATCC13032 strain determined as described above, and the known *gltA* gene and amino acid sequence of CS of the *Corynebacterium glutamicum* ATCC13032 strain (*Microbiol., 140*, 1817-1828 (1994)). The results are shown in Table 10 (for nucleotide sequences) and Table 11 (for amino acid sequences).

Table 10: Homology of nucleotide sequences of various *gltA* genes

	ATCC13869	ATCC13032	AJ12310
ATCC13869	-	99.5%	85.7%
ATCC13032	-	-	85.6%
AJ12310	-	-	-

Table 11: Homology of amino acid sequences of various CS

	ATCC13869	ATCC13032	AJ12310
ATCC13869	-	99.3%	92.1%
ATCC13032	-	-	92.1%
AJ12310	-	-	-

Example 3: Acquisition of *scrB* gene of *Corynebacterium thermoaminogenes*

Since an *scrB* gene fragment was obtained from the *Corynebacterium thermoaminogenes* AJ12309 strain as shown in Example 1, it was attempted to obtain the total sequence of the gene. First, a partial fragment was obtained in the same manner as in Example 1 using the primers shown in SEQ ID NO: 45 and SEQ ID NO: 46. These primers were synthesized based on the *scrB* sequence of the *Brevibacterium lactofermentum* 2256 strain (Japanese Patent Laid-open No. 08-196280/1996).

Separately, chromosomal DNA was prepared from the AJ12309 strain by using Bacterial Genome DNA Purification Kit (Advanced Genetic Technologies Corp.). Sterilized water was added to 0.5 μg of this chromosomal

DNA, 50 pmol each of the aforementioned primers, 4 μl of dNTP mixture (2.5 mM each), 5 μl of 10 x Z-Taq Buffer (Takara Shuzo) and 2 U of Z-Taq (Takara Shuzo) to prepare a PCR reaction mixture in a total volume of 50 μl. PCR was performed with a cycle of denaturation at 98°C for 5 seconds, association at 50°C for 10 seconds and extension reaction at 72°C for 20 seconds, which was repeated for 30 cycles, by using the above reaction mixture and a thermal cycler GeneAmp PCR System 9600 (PE) to amplify a partial fragment of *scrB* of about 600 bp.

Then, the total sequence of *scrB* was determined by using an LA PCR in vitro Cloning Kit (Takara Shuzo). All of the procedure was performed in accordance with the protocol attached to the LA PCR in vitro Cloning Kit. Based on the obtained partial sequence, primers shown in SEQ ID NOS: 97, 98, 99 and 100 were synthesized. For the first PCR reaction for sequencing an upstream region, the primers shown in SEQ ID NOS: 95 and 97 and chromosomal DNA of AJ12309 strain digested with *Eco*T14I as a template DNA were used. For the second PCR reaction, the primers shown in SEQ ID NOS: 96 and 98 were used. For the first PCR reaction for sequencing a downstream region, the primers shown in SEQ ID NOS: 95 and 99 and chromosomal DNA of AJ12309 strain digested with *Sal*I (Takara Shuzo) as a template DNA were used. For the second PCR reaction, the primers shown in SEQ ID

NOS: 96 and 100 were used. By the above procedure, a sequence of a full length of 1656 bp containing ORF of *scrB* was determined. This nucleotide sequence is shown in SEQ ID NO: 93, and a deduced amino acid sequence is shown in SEQ ID NO: 94.

Example 4: Examination of thermal stability of isocitrate lyase, phosphofructokinase, phosphoenolpyruvate carboxylase, aconitase, isocitrate dehydrogenase and 2-oxoglutarate dehydrogenase

Thermal stability was investigated for the following enzymes derived from *Corynebacterium thermoaminogenes*. In this Example, protein concentrations were measured by the Bradford method (Bio-Rad Protein Assay Kit was used) using bovine serum albumin as a standard protein. Further, measurement of absorbance was performed by using HITACHI U-2000 (Hitachi) unless otherwise indicated.

<1> Isocitrate lyase

Thermal stability of activity of isocitrate lyase (henceforth also referred to as "ICL") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and ICL derived from the *Brevibacterium lactofermentum* 2256 strain (ATCC13869) was investigated. For the activity measurement, used were cells of which culture in a medium having the composition mentioned in Table 2 was

terminated before all of the carbon source was completely consumed. The method of the activity measurement was one described in Dieter J. Reinscheid *et al.*, *J. Bacteriol.*, *176* (12), 3474 (1994). Specifically, the cells were washed with 50 mM Tris buffer (pH 7.3), suspended in the same buffer, and disrupted by sonication (INSONATOR 201M produced by KUBOTA was used, 200 W, 5 minutes). After the sonication, the suspension was centrifuged (13000 x g, 30 minutes) to remove undisrupted cells to prepare a crude enzyme solution.

The crude enzyme solution was added to a reaction system containing 50 mM MOPS-NaOH (pH 7.3), 5 mM dithiothreitol, 15 mM $MgCl_2$, 1 mM EDTA, 5 mM D-threo-isocitrate, 0.2 mM NADH and 18 U of LDH (lactate dehydrogenase), and absorbance at 340 nm at various temperatures (30, 40, 50, 60 or 70°C) was measured by a Hitachi spectrophotometer U-3210. The measurement results for various reaction temperatures were shown in Fig. 5. Further, the crude enzyme solution was pretreated at 50°C (pretreatment time: 5 minutes or 15 minutes), and the activity was measured at 37°C. The results are shown in Fig. 6.

As a result, ICL of the AJ12310 strain showed the maximum activity at 60°C, whereas ICL of the 2256 strain showed the maximum activity around 50°C. Further, while ICL of the 2256 strain was completely inactivated after the pretreatment for 5 minutes, ICL of the AJ12310

strain maintained half of the activity after the pretreatment for 5 minutes. Thus, the stability of ICL of the AJ12310 strain at high temperatures was confirmed.

Table 12 Composition of medium for ICL activity measurement

Component	Concentration
$(NH_4)_2SO_4$	5 g/l
Urea	5 g/l
KH_2PO_4	0.5 g/l
K_2HPO_4	0.5 g/l
MOPS	20.9 g/l
$MgSO_4 \cdot 7H_2O$	0.25 g/l
$CaCl_2 \cdot 7H_2O$	10 mM
$CuSO_4 \cdot 7H_2O$	0.2 mg/l
Biotin	0.2 mg/l
$MnSO_4 \cdot 7H_2O$	10 mg/l
$FeSO_4 \cdot 7H_2O$	10 mg/l
$ZnSO_4 \cdot 7H_2O$	1 mg/l
Acetic acid	4%

<2> Phosphofructokinase

Thermal stability of activity of phosphofructokinase (henceforth also referred to as "PKF") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and PKF derived from the *Brevibacterium lactofermentum* 2256 strain was investigated. For the activity measurement, used were cells of which culture in a medium having the composition mentioned in Table 13 was terminated before all of the saccharide was completely consumed. The method of the activity measurement was one described in Michiko Mori *et al.*,

Agric. Biol. Chem., *51* (10), 2671 (1994). Specifically, the cells were washed with 0.1 M Tris buffer (pH 7.5), suspended in the same buffer, and disrupted by sonication (INSONATOR 201M produced by KUBOTA was used, 200 W, 5 minutes). After the sonication, the suspension was centrifuged (13000 x g, 30 minutes) to remove undisrupted cells to obtain a crude enzyme solution.

The crude enzyme solution was added to a reaction system containing 100 mM Tris buffer (pH 7.5), 0.2 mM NADH, 10 mM $MgCl_2$, 2 mM NH_4Cl, 10 mM KCl, 0.2 mM phosphoenolpyruvic acid, 6.4 mM fructose-6-phosphate, 1 mM ATP and 40 μg of LDH/PK (pyruvate kinase), and absorbance at 340 nm was measured at various temperatures (30, 40, 50, 60 or 70°C) by a Hitachi spectrophotometer U-3210. The measurement results for various reaction temperatures were shown in Fig. 7. Further, the crude enzyme solution was pretreated at 50°C (pretreatment time: 1, 3, 5 or 10 minutes), and the activity was measured at 37°C. The results are shown in Fig. 8.

As a result, PKF of the AJ12310 strain showed the maximum activity around 50°C, whereas PKF of the 2256 strain showed the maximum activity around 30°C. Thus, it was confirmed that the optimum temperature of PKF of the AJ12310 strain resided in a high temperature region.

Table 13 Composition of medium for PFK activity measurement

Component	Concentration
Polypeptone	20 g/l
Yeast extract	20 g/l
Sodium chloride	5 g/l
Glucose	20 g/l

<3> Phosphoenolpyruvate carboxylase

Thermal stability of activity of phosphoenolpyruvate carboxylase (henceforth also referred to as "PEPC") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and PEPC of the *Brevibacterium lactofermentum* 2256 strain was examined.

Cells of the AJ12310 strain grown on CM-2B agar medium were inoculated to a 500-ml volume flask containing 20 ml of a medium for flask (8 g/dl of Glucose, 0.1 g/dl of KH_2PO_4, 0.04 g/dl of $MgSO_4 \cdot H_2O$, 1 mg/dl of $FeSO_4 \cdot 7H_2O$, 5 mg/dl of $MnSO_4 \cdot 4H_2O$, 3 g/dl of $(NH_4)_2SO_4$, 48 mg/dl of TN (soybean protein hydrolysis solution), 200 μg/L of vitamin B_1, 300 μg/L of biotin, 50 μl/l of GD-113 (antifoaming agent), 5 g/dl of $CaCO_3$ (Official regent, separately sterilized), pH 8.0 (adjusted with KOH)), and cultured at 37°C. Cells of the 2256 strain grown on CM-2B agar medium were similarly cultured at 31.5°C.

The above culture broth in which the cells were grown to the logarithmic growth phase was centrifuged at 1000 rpm for 1 minute to remove $CaCO_3$, and the cells

were washed 3 times with washing buffer (100 mM Tris/HCl pH 8.0, 10 mM $MgSO_4$, 1 mM DTT, 20% glycerol), sonicated to disrupt the cells, and centrifuged at 15 krpm for 10 minutes to remove cell debris. The supernatant was further centrifuged at 60 krpm for 1 hour to obtain a crude enzyme solution as the supernatant.

By using the above crude enzyme solution, optimum reaction temperature and thermal stability of the PEPC activity were investigated. The measurement of PEPC activity was performed by adding the crude enzyme solution to a reaction mixture (100 mM Tris/H_2SO_4 (pH 8.5), 5 mM phosphoenolpyruvic acid, 10 mM $KHCO_3$, 0.1 mM acetyl-CoA, 0.15 mM NADH, 10 mM $MgSO_4$, 10 U of malate dehydrogenase, 0.1 mM DTT), and measuring change of the absorbance at 340 nm in 800 μl of reaction volume.

The PEPC activity measured at various reaction temperatures is shown in Fig. 9. While the activity of the 2256 strain markedly decreased at 40°C, the AJ12310 strain showed substantially no decrease of the activity even at 40°C.

Then, the thermal stability of PEPC was investigated. The crude enzyme solution was left at 45°C for 0-20 minutes before the reaction, and then the enzyme activity was measured at 20°C. The results are shown in Fig. 10. As clearly seen from the results, whereas the PEPC activity of the 2256 strain was substantially lost after the heat treatment for 10

minutes, PEPC of the AJ12310 strain maintained the activity even after the heat treatment for 20 minutes.

These results demonstrated the stability of PEPC of the AJ12310 strain at a high temperature.

<4> Aconitase

Aconitase (henceforth also referred to as "ACN") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and ACN derived from the *Brevibacterium lactofermentum* 2256 strain were measured, and thermal stability thereof was examined.

Cells of the AJ12310 strain grown on CM-2B agar medium were inoculated to a 500-ml volume flask containing 20 ml of a medium for flask having the same composition as mentioned in <3>, and cultured at 37°C. Cells of the 2256 strain grown on CM-2B agar medium were similarly cultured at 31.5°C.

The above culture broth in which the cells were grown to the logarithmic growth phase was centrifuged at 1000 rpm for 1 minute to remove $CaCO_3$, and the cells were washed 3 times with 50 mM Tris/HCl pH 7.5, sonicated to disrupt the cells, and centrifuged at 15 krpm for 10 minutes to obtain a crude enzyme solution as the supernatant.

By using the above crude enzyme solution, optimum reaction temperature and thermal stability of ACN activity were investigated. The measurement of ACN

activity was performed by adding the crude enzyme solution to a reaction mixture (20 mM Tris/HCl (pH7.5), 50 mM NaCl, 20 mM isocitrate·3Na), and measuring change of the absorbance at 240 nm in 800 μl of reaction volume.

The ACN activity measured at various reaction temperatures is shown in Fig. 11. The AJ12310 strain showed higher activity at a higher temperature compared with the 2256 strain.

Then, the thermal stability of ACN was investigated. The crude enzyme solution was left at 50°C for 0-15 minutes before the reaction, and then the enzyme activity was measured at 30°C. The results are shown in Fig. 12. As clearly seen from the results, ACN of the AJ12310 strain showed less activity decrease due to the heat treatment compared with ACN of the 2256 strain.

These results demonstrated the stability of ACN of the AJ12310 strain at a high temperature.

<5> Isocitrate dehydrogenase

Thermal stability of activity of isocitrate dehydrogenase (henceforth also referred to as "ICDH") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and ICDH derived from the *Brevibacterium lactofermentum* 2256 strain was examined.

Cells of the AJ12310 strain grown on CM-2B agar medium were inoculated to a 500-ml volume flask

containing 20 ml of a medium for flask having the same composition as mentioned in <3>, and cultured at 37°C. Cells of the 2256 strain grown on CM-2B agar medium were similarly cultured at 31.5°C.

The above culture broth in which the cells were grown to the logarithmic growth phase was centrifuged at 1000 rpm for 1 minute to remove $CaCO_3$, and the cells were washed 3 times with 50 mM Tris/HCl pH 7.5, sonicated to disrupt the cells, and centrifuged at 15 krpm for 10 minutes to obtain a crude enzyme solution as the supernatant.

By using the above crude enzyme solution, optimum reaction temperature and thermal stability of ICDH activity were investigated. The measurement of ICDH activity was performed by adding the crude enzyme solution to a reaction mixture (35 mM Tris/HCl, 0.35 mM EDTA (pH 7.5), 1.5 mM $MnSO_4$, 0.1 mM NADP, 1.3 mM isocitrate·3Na), and measuring change of the absorbance at 340 nm in 800 μl of reaction volume.

The ICDH activity measured at various reaction temperatures is shown in Fig. 13. While the activity of the 2256 strain markedly decreased at 70°C, substantially no activity decrease was observed even at 70°C for the AJ12310 strain.

Then, the thermal stability of ICDH was investigated. The crude enzyme solution was left at 45°C for 0-15 minutes before the reaction, and then the

enzyme activity was measured at 30°C. The results are shown in Fig. 14. As clearly seen from the results, while only about 15% of residual activity was observed after the heat treatment for 15 minutes for the 2256 strain, about 60% of residual ICDH activity was observed for the AJ12310 strain.

These results demonstrated the stability of ICDH of the AJ12310 strain at a high temperature.

<6> 2-Oxoglutarate dehydrogenase

2-Oxoglutarate dehydrogenase (henceforth also referred to as "ODHC") derived from the *Corynebacterium thermoaminogenes* AJ12310 strain and ODHC derived from the *Brevibacterium lactofermentum* 2256 strain were measured, and thermal stability thereof was examined.

For the activity measurement, used were cells of which culture in a medium having the composition mentioned in Table 14 was terminated before all of the saccharide was completely consumed. The method of the activity measurement was one described in Isamu Shiio et al., Agric. Biol. Chem., 44 (8), 1897 (1980). Specifically, the cells were washed with 0.2% potassium chloride, suspended in 100 mM TES-NaOH (pH 7.5), 30% glycerol solution, and disrupted by sonication (INSONATOR 201M produced by KUBOTA was used, 200 W, 5 minutes). After the disruption by sonication, the suspension was centrifuged (13000 x g, 30 minutes) to

remove undisrupted cells, and subjected to gel filtration using the same buffer and Sephadex-G25 to prepare a crude enzyme solution.

The crude enzyme solution was added to a reaction system containing 100 mM TES-NaOH (pH 7.7), 5 mM $MgCl_2$, 0.2 mM Coenzyme A, 0.3 mM cocarboxylase, 1 mM α-ketoglutaric acid, 3 mM L-cysteine and 1 mM acetylpyridine-adenine dinucleotide, and absorbance at 365 nm was measured at various temperatures (30, 40, 50, 60 or 70°C) by a Hitachi spectrophotometer U-3210. The crude enzyme solution was pretreated at 50°C (pretreatment time: 1, 3, 5 or 10 minutes), and the activity was measured at 37°C. The results are shown in Fig. 15.

As a result, while ODHC of the 2256 strain was completely inactivated by the pretreatment for 10 minutes, ODHC of the AJ12310 strain showed substantially constant activity irrespective of the pretreatment time, and thus its stability against high temperature treatment was confirmed.

Table 14 Composition of medium for ODHC activity measurement

Component	Concentration
Glucose	80 g/l
KH_2PO_4	1 g/l
$MgSO_4 \cdot 7H_2O$	0.4 g/l
$FeSO_4 \cdot 7H_2O$	0.01 g/l
$MnSO_4 \cdot 7H_2O$	0.05 g/l
$(NH_4)_2SO_4$	30 g/l
Soybean protein hydrolysate	480 mg/l
Thiamin hydrochloride	200 μg/l
Biotin	300 μg/l

Example 5: Impartation of sucrose assimilating ability by gene transfer of *scrB* gene

Since the *Corynebacterium thermoaminogenes* AJ12310 strain did not have invertase activity and sucrose assimilating property, it was investigated if sucrose assimilating ability could be imparted to it by transferring the *scrB* gene of the AJ12309 strain to the strain.

<1> Production of plasmid carrying *scrB* derived from *Corynebacterium thermoaminogenes* AJ12309 strain

To obtain an *scrB* gene fragment, the primers shown in SEQ ID NOS: 101 and 102 were synthesized, of which both ends were ligated with *Sma*I sequences, based on the nucleotide sequence shown in SEQ ID NO: 93. Sterilized water was added to 0.5 μg of chromosomal DNA of the 12309 strain, 50 pmol each of the aforementioned

oligonucleotides, 4 μl of dNTP mixture (2.5 mM each), 5 μl of 10 x Pyrobest Buffer (Takara Shuzo) and 2 U of Pyrobest polymerase (Takara Shuzo) to prepare a PCR reaction mixture in a total volume of 50 μl. PCR was performed with a cycle of denaturation at 98°C for 10 seconds, association at 55°C for 30 seconds and extension reaction at 72°C for 2 minutes, which was repeated for 30 cycles, by using the above reaction mixture and a thermal cycler GeneAmp PCR System 9600 (PE) to amplify a fragment of about 1.7 kb containing *scrB* ORF.

Then, the above amplified fragment was digested with *Sma*I (Takara Shuzo), and ligated to plasmid pSAC4 containing a dephosphorylated replication origin functioning in coryneform bacteria, which had been digested with *Sma*I, to prepare pSCR155. The construction of pSCR155 is shown in Fig. 16. pSAC4 was produced as follows. In order to make the vector for *Escherichia coli* pHSG399 (Takara Shuzo) autonomously replicable in coryneform bacteria, the replication origin (Japanese Patent Laid-open No. 5-7491/1993) derived from the already obtained plasmid pHM1519 autonomously replicable in coryneform bacteria (Miwa, k.et al., Agric. Biol. Chem., 48 (1984) 2901-2903) was introduced into it. Specifically, pHM1519 was digested with restriction enzymes *Bam*HI and *Kpn*I, and the obtained fragment containing the replication origin was

blunt-ended by using a Blunting kit produced by Takara Shuzo and inserted into pHSG399 at the *Sal*I site by using an *Sal*I linker (produced by Takara Shuzo) to obtain pSAC4.

<2> Transfer of plasmid carrying *scrB* gene into AJ12310 strain

pSCR155 produced above and plasmid pSSM30BS (Japanese Patent Laid-open No. 08-196280/1996) carrying the *scrB* gene derived from *Brevibacterium lactofermentum* were introduced into the *Corynebacterium thermoaminogenes* AJ12310 strain. The transformation was performed according to the following procedure. The cells were inoculated to CM-2B medium containing 20% sucrose in such an amount that OD_{660} of the medium should become 0.1, and cultured at 37°C with shaking until the OD_{660} become 0.3. Lysozyme was added to the medium at a concentration of 100 μg/ml, and the cells were further cultured for 2 hours. The cells were washed three times with 20% sucrose, suspended in 20% sucrose, added with the plasmid collected from *Escherichia coli* JM110, mixed sufficiently, and applied with an electric pulse (18 kV/cm, 300 msec) to be introduced with the DNA. After the cells were subjected to restoration culture overnight in CM-2B medium containing 20% sucrose, transformants were selected on CM-2B agar medium containing 5 μg/ml of chloramphenicol. Specifically,

the transformation was performed by the electric pulse method (Japanese Patent Laid-open No. 12-204236/2000, and the selection of transformants was performed on CM2B plate medium containing 5 μg/ml of chloramphenicol at 37°C. As a result, any transformant harboring the plasmid pSSM30BS carrying *scrB* derived from *Brevibacterium lactofermentum* was not obtained, but only a transformant harboring the plasmid pSCR155 carrying *scrB* derived from *Corynebacterium thermoaminogenes* was obtained. This strain was designated as AJ12310/pSCR155.

<3> Evaluation of culture of AJ12310/pSCR155 strain using sucrose as sugar source.

AJ12310/pSCR155 prepared above was inoculated to a medium having the composition shown in Table 15, and cultured at 37°C for 22 hours with shaking. The absorbance (OD) and residual sugar (RS) of the medium were measured after the culture. The results are shown in Table 16. As a result, it was confirmed that, while the AJ12310 strain could not assimilate sucrose and hence could not grow, the *scrB* gene introduced strain, the AJ12310/pSCR155 strain, became to be able to assimilate sucrose.

Table 15 Medium composition

Medium composition	Concentration
Sucrose	60 g/l
KH_2PO_4	1 g/l
$MgSO_4 \cdot 7H_2O$	0.4 g/l
$FeSO_4 \cdot 7H_2O$	0.01 g/l
$MnSO_4 \cdot 7H_2O$	0.01 g/l
$(NH_4)_2SO_4$	30 g/l
Soybean protein hydrolysate	480 mg/l
Thiamin hydrochloride	200 μg/l
Biotin	300 μg/l

Table 16 Result of sucrose culture

	OD (x 51)	RS (g/l)
2256	1.292	0.00
AJ12310	0.058	60.00
AJ12310/pSCR155	1.571	0.84

Example 6: L-glutamic acid production by *pdhA* gene-amplified strain

<1> Construction of plasmid pPDHA-2 carrying *pdhA*

The *pdhA* gene derived from the *Corynebacterium thermoaminogenes* AJ12310 strain was obtained by screening of a plasmid library. Specifically, PCR was performed with the conditions shown in Example 1, Table 4, using a plasmid library mixture as a template, and a clone p21A was selected, from which a DNA fragment of the same size is amplified as obtained in PCR using chromosomal DNA as a template. The DNA sequence of this plasmid was determined to confirm that the full length of *pdhA* was contained in it.

p21A was digested with *Xba*I and *Kpn*I to excise a DNA fragment of 4 kb containing the full length of the *pdhA* gene and a promoter region. This DNA fragment containing the *pdhA* gene was inserted into the *Xba*I and *Kpn*I sites of pHSG299 (Takara Shuzo). Then, this plasmid was digested with *Xba*I, and a fragment obtained by digesting pXK4 with *Xba*I was inserted to prepare pPDHA-2. The construction process of pPDHA-2 is shown in Fig. 17. A DNA Ligation Kit Ver.2 (Takara Shuzo) was used for the ligation reaction, and *Escherichia coli* JM109 strain (Takara Shuzo) was used as the host of genetic manipulation. The aforementioned pXK4 was produced as follows. A shuttle vector pHK4 for coryneform bacteria and *Escherichia coli* (Japanese Patent Laid-open No. 5-7491/1993) was digested with restriction enzymes *Bam*HI and *Kpn*I to obtain a DNA fragment containing the replication origin, and the obtained fragment was blunt-ended by using a DNA blunting kit (Blunting Kit produced by Takara Shuzo), ligated to an *Xba*I linker (produced by Takara Shuzo) and inserted into pHSG299 at the *Xba*I site to obtain the plasmid pKX4.

<2> Transfer of plasmid carrying *pdhA* gene into AJ12310 strain

The plasmid pPDHA-2 produced above was introduced into the *Corynebacterium thermoaminogenes* AJ12310 strain

to prepare a *pdhA* gene-amplified strain. The transformation was performed in the same manner as Example 5, and a transformant was selected on CM-2B agar medium containing 25 μg/ml kanamycin to obtain AJ12310/pPDHA-2 strain.

<3> L-glutamic acid production by *pdhA*-amplified strain

The AJ12310 strain and the *pdhA* gene-amplified strain obtained above, AJ12310/pPDHA-2 strain, both of which were grown on CM-2B agar medium, were each inoculated to a 500-ml volume flask containing 20 ml of a medium for seed culture flask shown in Table 17, and cultured at 37°C with shaking until glucose was completely consumed. 2 ml of this culture broth was inoculated into 500 ml-volume flask containing 20 ml of a medium for main culture flask shown in Table 17, and cultured as main culture at 37°C and 44°C. The main culture was continued until glucose was completely consumed. After the culture, OD_{620} of the medium and accumulated amount of L-glutamic acid were measured to examine the effect of the gene amplification on the cell formation and production of glutamic acid. The measurement of OD was performed by using a spectrophotometer HITACHI U-2000 (Hitachi), and L-glutamic acid concentration was measured by using a glutamic acid analyzer AS-210 (Asahi Chemical Industry). The results are shown in Fig. 18.

The *pdhA* gene-amplified strain, AJ12310/pPDHA-2 strain, showed increased L-glutamic acid accumulation and increased OD compared with the AJ12310 strain, and thus it became clear that the amplification of the *pdhA* gene was effective for L-glutamic acid production.

Table 17 Medium for evaluation of *pdhA*-amplified strain

Medium composition	Seed culture	Main culture
Sucrose	30 g/l	60 g/l
KH_2PO_4	1 g/l	1 g/l
$MgSO_4 \cdot 7H_2O$	0.4 g/l	0.4 g/l
$FeSO_4 \cdot 7H_2O$	0.01 g/l	0.01 g/l
$MnSO_4 \cdot 7H_2O$	0.01 g/l	0.01 g/l
$(NH_4)_2SO_4$	15 g/l	30 g/l
Soybean protein hydrolysate	480 mg/l	480 mg/l
Thiamin hydrochloride	200 μg/l	200 μg/l
Biotin	10 μg/l	
AZ-20R (anti-foaming agent)	20 μg/l	20 μg/l
$CaCO_3$ (separately sterilized)	50 g/L	50 g/L
pH 8.0 (adjusted with KOH)		

Example 7: L-glutamic acid production by *icd* gene-amplified strain

<1> Construction of plasmid pICD-4 carrying *icd* derived from *Corynebacterium thermoaminogenes* AJ12310 strain

Based on the *icd* gene sequence of the AJ12310 strain shown in SEQ ID NO: 29, the primers shown in SEQ ID NO: 103 and SEQ ID NO: 104 were synthesized. A *Bgl*II site was introduced into 5′ end of the both primers.

Separately, genomic DNA of the *Corynebacterium thermoaminogenes* AJ12310 strain was prepared by using a Genomic DNA Purif. Kit (Edge BioSystems). Sterilized water was added to the genome DNA as a template, 100 pmol each of the aforementioned primers, 8 μl of dNTP mixture (2.5 mM each), 10 μl of 10 x Pyrobest Buffer II (Takara Shuzo) and 2.5 U of Pyrobest polymerase (Takara Shuzo) to prepare a PCR reaction mixture in a total volume of 100 μl. PCR was performed with a cycle of denaturation at 98°C for 10 seconds, association at 55°C for 1 minute and extension reaction at 72°C for 4 minutes, which was repeated for 30 cycles, by using the above reaction mixture and a thermal cycler TP240 (Takara Shuzo) to amplify a DNA fragment of about 3.3 kb containing the *icd* gene and its promoter.

Then, this DNA fragment containing the *icd* gene was digested with *Bgl*II, and ligated to pHSG299 (Takara Shuzo) at the *Bam*HI site. This plasmid was then treated with *Xba*I, and a fragment obtained by digesting pXK4 with *Xba*I was inserted into the plasmid to construct pICD-4. The construction procedure of pICD-4 is shown in Fig. 19. A DNA Ligation Kit Ver.2 (Takara Shuzo) was used for the ligation reaction, and *Escherichia coli* JM109 strain (Takara Shuzo) was used as the host of genetic manipulation.

<2> Transfer of plasmid carrying *icd* gene into AJ12310

strain

The plasmid pICD-4 produced above was introduced into the *Corynebacterium thermoaminogenes* AJ12310 strain to prepare an *icd* gene-amplified strain. The transformation was performed in the same manner as Example 5, and a transformant was selected on CM-2B agar medium containing 25 μg/ml kanamycin to obtain AJ12310/pICD-4 strain.

<3> L-glutamic acid production by *icd*-amplified strain

Culture evaluation was performed for the AJ12310 strain and the *icd*-amplified strain thereof, AJ12310/pICD, by the culture method described in Example 6. The results are shown in Fig. 20. The *icd* gene-amplified strain AJ12310/pICD-4 strain showed increased L-glutamic acid accumulation and increased OD compared with the AJ12310 strain, and thus it became clear that the amplification of the *icd* gene was effective for L-glutamic acid production.

Example 8: L-glutamic acid production by *gdh* gene-amplified strain

<1> Construction of plasmid carrying *gdh* derived from *Corynebacterium thermoaminogenes* AJ12310 strain

Based on the *gdh* gene sequence of the AJ12310 strain shown in SEQ ID NO: 79, the primers shown in SEQ ID NO: 105 and SEQ ID NO: 106 were synthesized.

Sep

arately, chromosomal DNA of the AJ12310 strain was prepared by using a Bacterial Genome DNA Purification Kit (Advanced Genetic Technologies Corp.). Sterilized water was added to 0.5 μg of this chromosomal DNA, 10 pmol each of the aforementioned oligonucleotides, 8 μl of dNTP mixture (2.5 mM each), 5 μl of 10 x LA Taq Buffer (Takara Shuzo) and 2 U of LA Taq (Takara Shuzo) to prepare a PCR reaction mixture in a total volume of 50 μl. PCR was performed with a cycle of denaturation at 94°C for 30 seconds, association at 55°C for 1 second and extension reaction at 72°C for 3 minutes, which was repeated for 30 cycles, by using the above reaction mixture and a thermal cycler TP240 (Takara Shuzo) to amplify a DNA fragment of about 2 kb containing the *gdh* gene and its promoter. The obtained amplified fragment was digested with *Pst*I (Takara Shuzo), mixed with pHSG299 (Takara Shuzo) fully digested with *Pst*I and ligated to it. A DNA Ligation Kit Ver.2 produced by Takara Shuzo was used for the ligation reaction. After the ligation, competent cells of *Escherichia coli* JM109 (produced by Takara Shuzo) were transformed with the ligation product, plated on L medium (10 g/l of Bacto-trypton, 5 g/l of Bacto-yeast extract, 5 g/l of NaCl, 15 g/l of agar, pH 7.2) containing 10 μg/ml of IPTG (isopropyl-β-D-thiogalactopyranoside), 40 μg/ml of X-Gal (5-bromo-4-chloro-3-indolyl-β-D-galactoside) and 40

μg/ml of chloramphenicol, and cultured overnight. The emerged white colonies were picked up and subjected to single colony separation to obtain transformants.

Plasmids were prepared from the transformants by the alkali method (Text for Bioengineering Experiments, Edited by the Society for Bioscience and Bioengineering, Japan, p.105, Baifukan, 1992) and their restriction maps were prepared. A plasmid having a restriction map equivalent to that shown in Fig. 21 was designated as pHSG299YGDH.

A replication origin that functions in coryneform bacteria was introduced into this pHSG299YGDH. Specifically, pXC4 was digested with a restriction enzyme *Xba*I to obtain a fragment containing a replication origin derived from pHM1519, and it was mixed with pHSG299YGDH fully digested with *Xba*I and ligated to it. Plasmids were prepared in the same manner as above and a plasmid having a restriction map equivalent to that shown in Fig. 21 was designated as pYGDH. pXC4 was constructed in the same manner as that for pXK4 mentioned in Example 6 except that pHSG399 (Cm^r) was used instead of pHSG299.

<2> Transfer of plasmid carrying *gdh* gene into AJ12310

The plasmid produced above was introduced into the *Corynebacterium thermoaminogenes* AJ12310 strain to prepare a *gdh* gene-amplified strain. The transformation

was performed in the same manner as Example 5, and a transformant was selected on CM-2B agar medium containing 25 μg/ml kanamycin at 31°C to obtain AJ12310/pYGDH.

<3> L-glutamic acid production by *gdh*-amplified strain

The AJ12310 strain and the *gdh* gene-amplified strain obtained above, AJ12310/pYGDH strain, both of which were grown on CM-2B agar medium, were each inoculated to a 500-ml volume flask containing 20 ml of a medium for seed culture flask shown in Table 18, and cultured at 37°C with shaking until glucose was completely consumed. 2 ml of this culture broth was inoculated into 500 ml-volume flask containing 20 ml of a medium for main culture flask shown in Table 19, and cultured as main culture at 37°C and 44°C. The main culture was continued until glucose was completely consumed. After completion of the culture, OD_{620} of the medium and accumulated amount of L-glutamic acid were measured to examine the effect of the gene amplification on the cell formation and production of glutamic acid. The measurement of OD was performed by using a spectrophotometer HITACHI U-2000 (Hitachi), and L-glutamic acid concentration was measured by using a glutamic acid analyzer AS-210 (Asahi Chemical Industry).

Table 18 Composition of medium for seed culture

Medium composition	Concentration
Glucose	30 g/l
Ammonium sulfate	15 g/l
KH_2PO_4	1 g/l
$MgSO_4 \cdot 7H_2O$	0.4 g/l
$FeSO_4 \cdot 7H_2O$	0.01 g/l
$MnSO_4 \cdot 7H_2O$	0.01 g/l
Soybean protein hydrolysate	0.48 g/l
Thiamin hydrochloride	200 μg/l
Biotin	10 μg/l
AZ20R	0.02 ml/l
$CaCO_3$ (separately sterilized)	1 g/L
pH 8.0 (adjusted with KOH)	

Table 19 Composition of medium for main culture

Medium composition	Concentration
Glucose	60 g/l
Ammonium sulfate	30 g/l
KH_2PO_4	1 g/l
$MgSO_4 \cdot 7H_2O$	0.4 g/l
$FeSO_4 \cdot 7H_2O$	0.01 g/l
$MnSO_4 \cdot 7H_2O$	0.01 g/l
Soybean protein hydrolysate	0.48 g/l
Thiamin hydrochloride	200 μg/l
AZ20R	0.02 ml/l
$CaCO_3$ (separately sterilized)	1 g/L
PH 8.0 (adjusted with KOH)	

The results of the culture are shown in Table 20 and Table 21. At 37°C, the *gdh*-amplified strain showed higher saccharide consuming rate, better growth and

higher attained OD compared with the parent strain, the AJ12310 strain. Moreover, both of the L-glutamic acid accumulation and the yield were markedly improved, *i*.e., 5-7%, at 37°C. Also at 44°C, the yield was improved, and the attained OD increased. On the other hand, it was confirmed that accumulation of α-ketoglutaric acid was decreased in the *gdh*-amplified strain. These results demonstrate that the amplification of *gdh* is effective for improvement in L-glutamic acid yield and reduction of byproduct.

Table 20 Culture result of *gdh*-amplified strain (37°C)

	OD_{620} (51x)	L-Glu accumulation (g/dl)	L-Glu yield (%)	α-KG (mg/dl)
AJ12310	0.58	1.74	30.7	53.9
AJ12310/PYGDH	0.65	2.23	39.3	4.1

Table 21 Culture result of *gdh*-amplified strain (44°C)

	OD_{620} (51x)	L-Glu accumulation (g/dl)	L-Glu yield (%)
AJ12310	0.63	1.70	26.7
AJ12310/pYGDH	0.71	1.79	27.8

Example 9: L-glutamic acid production by *gltA* gene-amplified strain

<1> Construction of plasmid carrying *gltA* gene derived from *Corynebacterium thermoaminogenes*

Based on the *gltA* gene sequence of the AJ12310 strain shown in SEQ ID NO: 89, the primers shown in SEQ

ID NO: 107 and SEQ ID NO: 108 were synthesized.

Separately, chromosomal DNA of the AJ12310 strain was prepared by using a Bacterial Genome DNA Purification Kit (Advanced Genetic Technologies Corp.). Sterilized water was added to 0.5 μg of this chromosomal DNA, 10 pmol each of the aforementioned oligonucleotides, 8 μl of dNTP mixture (2.5 mM each), 10 μl of 10 x Pyrobest-Taq Buffer (Takara Shuzo) and 2 U of Pyrobest Taq (Takara Shuzo) to prepare a PCR reaction mixture in a total volume of 100 μl. PCR was performed with a cycle of denaturation at 94°C for 30 seconds, association at 45°C for 30 seconds and extension reaction at 72°C for 3 minutes, which was repeated for 30 cycles, by using the above reaction mixture and a thermal cycler TP240 (Takara Shuzo) to amplify a DNA fragment of about 2 kb containing the *gltA* gene and its promoter. The obtained amplified fragment was digested with *Kpn*I (Takara Shuzo), mixed with pHSG299 (Takara Shuzo) fully digested with *Kpn*I and ligated to it. A DNA Ligation Kit Ver.2 produced by Takara Shuzo was used for the ligation reaction. After the ligation, competent cells of *Escherichia coli* JM109 (produced by Takara Shuzo) were transformed with the ligation product, plated on L medium (10 g/l of Bacto-trypton, 5 g/l of Bacto-yeast extract, 5 g/l of NaCl, 15 g/l of agar, pH 7.2) containing 10 μg/ml of IPTG (isopropyl-β-D-thiogalactopyranoside), 40 μg/ml of X-Gal (5-bromo-4-

chloro-3-indolyl-β-D-galactoside) and 40 μg/ml of chloramphenicol, and cultured overnight. The emerged white colonies were picked up and subjected to single colony separation to obtain transformants.

Plasmids were prepared from the transformants by the alkali method (Text for Bioengineering Experiments, Edited by the Society for Bioscience and Bioengineering, Japan, p.105, Baifukan, 1992) and their restriction maps were prepared. A plasmid having a restriction map equivalent to that shown in Fig. 22 was designated as pHSG299YCS.

A replication origin that is replicable in coryneform bacteria was introduced into this pHSG299YCS. Specifically, pXC4 was digested with a restriction enzyme *Xba*I to obtain a fragment containing a replication origin derived from pHM1519, and it was mixed with pHSG299YCS fully digested with *Xba*I and ligated to it. Plasmids were prepared in the same manner as above and a plasmid having a restriction map equivalent to that shown in Fig. 22 was designated as pYCS.

<2> Transfer of plasmid carrying *gltA* gene into AJ12310 strain

The plasmid produced above was introduced into the *Corynebacterium thermoaminogenes* AJ12310 strain to prepare a *gltA* gene-amplified strain. The

transformation was performed in the same manner as Example 5, and a transformant was selected on CM-2B agar medium containing 25 μg/ml kanamycin to obtain AJ12310/pYCS.

<3> L-glutamic acid production by *gltA*-amplified strain

The AJ12310 strain and the *gltA* gene-amplified strain obtained above, AJ12310/pYCS strain, both of which were grown on CM-2B agar medium, were cultured in the same manner as in Example 8. The results of the culture are shown in Table 22 and Table 23. Both at the culture temperatures, 37°C and 44°C, the CS-enhanced strain showed improved glutamic acid accumulation compared with the parent strain. Further, the *gltA*-amplified strain showed decreased L-aspartic acid and L-lysine, which are synthesized from oxaloacetic acid.

These results demonstrate that the amplification of *gltA* is effective for improvement of L-glutamic acid yield and reduction of byproduct.

Table 22 Culture result of *gltA*-amplified strain (37°C)

	L-Glu accumulation (g/dl)	Yield (%)	L-Asp accumulation (mg/dl)	L-Lys accumulation (mg/dl)
AJ12310	1.79	31.9	11.8	11.0
AJ12310/pYCS	2.04	36.5	8.1	7.3

Table 23 Culture result of *gltA*-amplified strain (44°C)

	OD	L-Glu accumulation (g/dl)	Yield (%)	L-Asp accumulation (mg/dl)	L-Lys Accumulation (mg/dl)
AJ12310	0.58	1.38	21.8	23.3	29.2
AJ12310/pYCS	0.65	1.84	28.8	14.1	17.2

[Explanation of Sequence Listing]

SEQ ID NO: 1: *aceA*, nucleotide sequence

SEQ ID NO: 2: *aceA*, amino acid sequence

SEQ ID NO: 3: *accBC*, nucleotide sequence

SEQ ID NO: 4: *accBC*, amino acid sequence

SEQ ID NO: 5: *dtsR1*, nucleotide sequence

SEQ ID NO: 6: *dtsR1*, amino acid sequence

SEQ ID NO: 7: *dtsR2*, nucleotide sequence

SEQ ID NO: 8: *dtsR2*, amino acid sequence

SEQ ID NO: 9: *pfk*, nucleotide sequence

SEQ ID NO: 10: *pfk*, amino acid sequence

SEQ ID NO: 11: *scrB* (AJ12340), nucleotide sequence

SEQ ID NO: 12: *scrB* (AJ12340), amino acid sequence

SEQ ID NO: 13: *scrB* (AJ12309), nucleotide sequence

SEQ ID NO: 14: *scrB* (AJ12309), amino acid sequence

SEQ ID NO: 15: *scrB* (AJ12310), nucleotide sequence

SEQ ID NO: 16: *gluABCD*, nucleotide sequence

SEQ ID NO: 17: *gluABCD*, amino acid sequence

SEQ ID NO: 18: *gluABCD*, amino acid sequence

SEQ ID NO: 19: *gluABCD*, amino acid sequence

SEQ ID NO: 20: *gluABCD*, amino acid sequence

SEQ ID NO: 21: *pdhA*, nucleotide sequence

SEQ ID NO: 22: *pdhA*, amino acid sequence

SEQ ID NO: 23: *pc*, nucleotide sequence

SEQ ID NO: 24: *pc*, amino acid sequence

SEQ ID NO: 25: *ppc*, nucleotide sequence

SEQ ID NO: 26: *ppc*, amino acid sequence

SEQ ID NO: 27: *acn*, nucleotide sequence

SEQ ID NO: 28: *acn*, amino acid sequence

SEQ ID NO: 29: *icd*, nucleotide sequence

SEQ ID NO: 30: *icd*, amino acid sequence

SEQ ID NO: 31: *lpd*, nucleotide sequence

SEQ ID NO: 32: *lpd*, amino acid sequence

SEQ ID NO: 33: *odhA*, nucleotide sequence

SEQ ID NO: 34: *odhA*, amino acid sequence

SEQ ID NO: 79: *gdh* (AJ12310), nucleotide sequence

SEQ ID NO: 80: *gdh* (AJ12310), amino acid sequence

SEQ ID NO: 81: *gdh* (2256), nucleotide sequence

SEQ ID NO: 82: *gdh* (2256), amino acid sequence

SEQ ID NO: 89: *gltA* (AJ12310), nucleotide sequence

SEQ ID NO: 90: *gltA* (AJ12310), amino acid sequence

SEQ ID NO: 91: *gltA* (2256), nucleotide sequence

SEQ ID NO: 92: *gltA* (2256), amino acid sequence

SEQ ID NO: 93: *scrB* (AJ12309), nucleotide sequence

SEQ ID NO: 94: *scrB* (AJ12309), amino acid sequence

Industrial Applicability

According to the present invention, genes coding

for enzymes of amino acid biosynthetic pathway derived from *Corynebacterium thermoaminogenes*, or genes coding for proteins involved in the amino acid uptake into cells.

The genes of the present invention can be utilized for the production of the aforementioned enzymes or proteins, or the breeding of amino acid producing bacteria.

What is claimed is:

1. A protein having the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence of SEQ ID NO: 2 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has isocitrate lyase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 5 minutes.

2. A protein having the amino acid sequence of SEQ ID NO: 4 or the amino acid sequence of SEQ ID NO: 4 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which is involved in acyl Co-A carboxylase activity and is derived from *Corynebacterium thermoaminogenes*.

3. A protein having the amino acid sequence of SEQ ID NO: 6 or the amino acid sequence of SEQ ID NO: 6 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has DtsR activity and is derived from *Corynebacterium thermoaminogenes*.

4. A protein having the amino acid sequence of SEQ ID NO: 8 or the amino acid sequence of SEQ ID NO: 8

including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has DtsR activity and is derived from *Corynebacterium thermoaminogenes*.

5. A protein having the amino acid sequence of SEQ ID NO: 10 or the amino acid sequence of SEQ ID NO: 10 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows phosphofructokinase activity at 60° C in an equivalent or higher degree compared with the activity at 30° C.

6. A protein having the amino acid sequence of SEQ ID NO: 94 or the amino acid sequence of SEQ ID NO: 94 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has activity for imparting sucrose assimilating ability to *Corynebacterium thermoaminogenes*.

7. A protein having any one of the amino acid sequences of SEQ ID NOS: 17-20 or the amino acid sequence of any one of SEQ ID NOS: 17-20 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has a function involved in glutamic acid uptake and is derived from *Corynebacterium thermoaminogenes*.

8. A protein having the amino acid sequence of SEQ ID NO: 22 or the amino acid sequence of SEQ ID NO: 22 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has pyruvate dehydrogenase activity and is derived from *Corynebacterium thermoaminogenes*.

9. A protein having the amino acid sequence of SEQ ID NO: 24 or the amino acid sequence of SEQ ID NO: 24 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has pyruvate carboxylase activity and is derived from *Corynebacterium thermoaminogenes*.

10. A protein having the amino acid sequence of SEQ ID NO: 26 or the amino acid sequence of SEQ ID NO: 26 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has phosphoenolpyruvate carboxylase activity and shows 50% or more of residual activity after a heat treatment at 45°C for 5 minutes.

11. A protein having the amino acid sequence of SEQ ID NO: 28 or the amino acid sequence of SEQ ID NO: 28 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues,

which has aconitase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 3 minutes.

12. A protein having the amino acid sequence of SEQ ID NO: 30 or the amino acid sequence of SEQ ID NO: 30 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has isocitrate dehydrogenase activity and shows 50% or more of residual activity after a heat treatment at 45°C for 10 minutes.

13. A protein having the amino acid sequence of SEQ ID NO: 32 or the amino acid sequence of SEQ ID NO: 32 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has dihydrolipoamide dehydrogenase activity and is derived from *Corynebacterium thermoaminogenes*.

14. A protein having the amino acid sequence of SEQ ID NO: 34 or the amino acid sequence of SEQ ID NO: 34 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which has 2-oxoglutarate dehydrogenase activity and shows 30% or more of residual activity after a heat treatment at 50°C for 10 minutes.

15. A protein having the amino acid sequence of SEQ ID NO: 80 in Sequence Listing or the amino acid sequence of SEQ ID NO: 80 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows glutamate dehydrogenase activity at 42°C in an equivalent or higher degree compared with the activity at 37°C.

16. A protein having the amino acid sequence of SEQ ID NO: 90 in Sequence Listing or the amino acid sequence of SEQ ID NO: 90 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, which shows citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.

17. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 2 or the amino acid sequence of SEQ ID NO: 2 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having isocitrate lyase activity.

18. The DNA according to Claim 17, which is a DNA defined in the following (a1) or (b1):

(a1) a DNA which comprises the nucleotide sequence of SEQ ID NO: 1 in Sequence Listing,

(b1) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 1 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having isocitrate lyase activity.

19. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 4 or the amino acid sequence of SEQ ID NO: 4 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and involved in acyl Co-A carboxylase activity.

20. The DNA according to Claim 19, which is a DNA defined in the following (a2) or (b2):

(a2) a DNA which comprises the nucleotide sequence of SEQ ID NO: 3 in Sequence Listing,

(b2) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 3 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein involved in acyl Co-A carboxylase activity.

21. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 6 or the amino acid sequence of SEQ ID NO: 6 including substitution, deletion, insertion, addition or inversion of one or

several amino acids residues, and having DtsR activity.

22. The DNA according to Claim 21, which is a DNA defined in the following (a3) or (b3):

(a3) a DNA which comprises the nucleotide sequence of SEQ ID NO: 5 in Sequence Listing,

(b3) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 5 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having DtsR activity.

23. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 8 or the amino acid sequence of SEQ ID NO: 8 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having DtsR activity.

24. The DNA according to Claim 23, which is a DNA defined in the following (a4) or (b4):

(a4) a DNA which comprises the nucleotide sequence of SEQ ID NO: 7 in Sequence Listing,

(b4) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 7 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having DtsR activity.

25. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 10 or the amino acid sequence of SEQ ID NO: 10 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having phosphofructokinase activity.

26. The DNA according to Claim 25, which is a DNA defined in the following (a5) or (b5):

(a5) a DNA which comprises the nucleotide sequence of SEQ ID NO: 9 in Sequence Listing,

(b5) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 9 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having phosphofructokinase activity.

27. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 93 or the amino acid sequence of SEQ ID NO: 93 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having invertase activity.

28. The DNA according to Claim 27, which is a DNA defined in the following (a6) or (b6):

(a6) a DNA which comprises the nucleotide sequence of SEQ ID NO: 93 in Sequence Listing,

(b6) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 93 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having invertase activity.

29. A DNA which codes for a protein having any one of the amino acid sequences of SEQ ID NOS: 17-20 or the amino acid sequence of any one of SEQ ID NOS: 17-20 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having a function involved in glutamic acid uptake.

30. The DNA according to Claim 29, which is a DNA defined in the following (a7) or (b7):

(a7) a DNA which comprises the nucleotide sequence of SEQ ID NO: 16 in Sequence Listing,

(b7) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 16 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having a function involved in glutamic acid uptake.

31. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 22 or the amino acid

sequence of SEQ ID NO: 22 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having pyruvate dehydrogenase activity.

32. The DNA according to Claim 31, which is a DNA defined in the following (a8) or (b8):

(a8) a DNA which comprises the nucleotide sequence of SEQ ID NO: 21 in Sequence Listing,

(b8) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 21 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having pyruvate dehydrogenase activity.

33. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 24 or the amino acid sequence of SEQ ID NO: 24 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having pyruvate carboxylase activity.

34. A DNA according to Claim 33, which is a DNA defined in the following (a9) or (b9):

(a9) a DNA which comprises the nucleotide sequence of SEQ ID NO: 23 in Sequence Listing,

(b9) a DNA which is hybridizable with the

nucleotide sequence of SEQ ID NO: 23 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having pyruvate carboxylase activity.

35. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 26 or the amino acid sequence of SEQ ID NO: 26 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having phosphoenolpyruvate carboxylase activity.

36. The DNA according to Claim 35, which is a DNA defined in the following (a10) or (b10):

(a10) a DNA which comprises the nucleotide sequence of SEQ ID NO: 25 in Sequence Listing,

(b10) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 25 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having phosphoenolpyruvate carboxylase activity.

37. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 28 or the amino acid sequence of SEQ ID NO: 28 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having aconitase

activity.

38. The DNA according to Claim 37, which is a DNA defined in the following (a11) or (b11):

(a11) a DNA which comprises the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing,

(b11) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having aconitase activity.

39. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 30 or the amino acid sequence of SEQ ID NO: 30 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having isocitrate dehydrogenase activity.

40. The DNA according to Claim 39, which is a DNA defined in the following (a12) or (b12):

(a12) a DNA which comprises the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing,

(b12) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 27 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein

having isocitrate dehydrogenase activity.

41. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 32 or the amino acid sequence of SEQ ID NO: 32 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having dihydrolipoamide dehydrogenase activity.

42. The DNA according to Claim 41, which is a DNA defined in the following (a13) or (b13):

(a13) a DNA which comprises the nucleotide sequence of SEQ ID NO: 31 in Sequence Listing,

(b13) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 31 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having dihydrolipoamide dehydrogenase activity.

43. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 34 or the amino acid sequence of SEQ ID NO: 34 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and having 2-oxoglutarate dehydrogenase activity.

44. The DNA according to Claim 43, which is a

DNA defined in the following (a14) or (b14):

(a14) a DNA which comprises the nucleotide sequence of SEQ ID NO: 33 in Sequence Listing,

(b14) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 33 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein having 2-oxoglutarate dehydrogenase activity.

45. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 80 in Sequence Listing or the amino acid sequence of SEQ ID NO: 80 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and showing glutamate dehydrogenase activity at 42°C in an equivalent or higher degree compared with the activity at 37°C.

46. The DNA according to Claim 45, which is a DNA defined in the following (a15) or (b15):

(a15) a DNA which comprises the nucleotide sequence of SEQ ID NO: 79 in Sequence Listing,

(b15) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 79 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein showing glutamate dehydrogenase activity at 42°C in an

equivalent or higher degree compared with the activity at 37°C.

47. A DNA which codes for a protein having the amino acid sequence of SEQ ID NO: 90 in Sequence Listing or the amino acid sequence of SEQ ID NO: 90 including substitution, deletion, insertion, addition or inversion of one or several amino acids residues, and showing citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.

48. The DNA according to Claims 47, which is a DNA defined in the following (a16) or (b16):

(a16) a DNA which comprises the nucleotide sequence of SEQ ID NO: 89 in Sequence Listing,

(b16) a DNA which is hybridizable with the nucleotide sequence of SEQ ID NO: 89 in Sequence Listing or a primer prepared based on the nucleotide sequence under a stringent condition, and codes for a protein showing citrate synthase activity at 37°C in an equivalent or higher degree compared with the activity at 23°C.

49. A method for producing L-amino acid, which comprises culturing a microorganism introduced with a DNA according to any one of Claims 17 to 48 in a medium to produce and accumulate L-amino acid in the medium,

and collecting the L-amino acid from the medium.

ABSTRACT

A plurality of primer sets are designed based on a region where conservation at the amino acid level is observed among various microorganisms for known gene sequences corresponding to a gene coding for an enzyme of the L-amino acid biosynthetic pathway derived from *Corynebacterium thermoaminogenes*, preferably an enzyme that functions at a higher temperature compared with that of *Corynebacterium glutamicum*. PCR is performed by using the primers and chromosomal DNA of *Corynebacterium thermoaminogenes* as a template. The primers with which an amplification fragment has been obtained are used as primers for screening to select a clone containing a target DNA fragment from a plasmid library of chromosomal DNA of *Corynebacterium thermoaminogenes*.

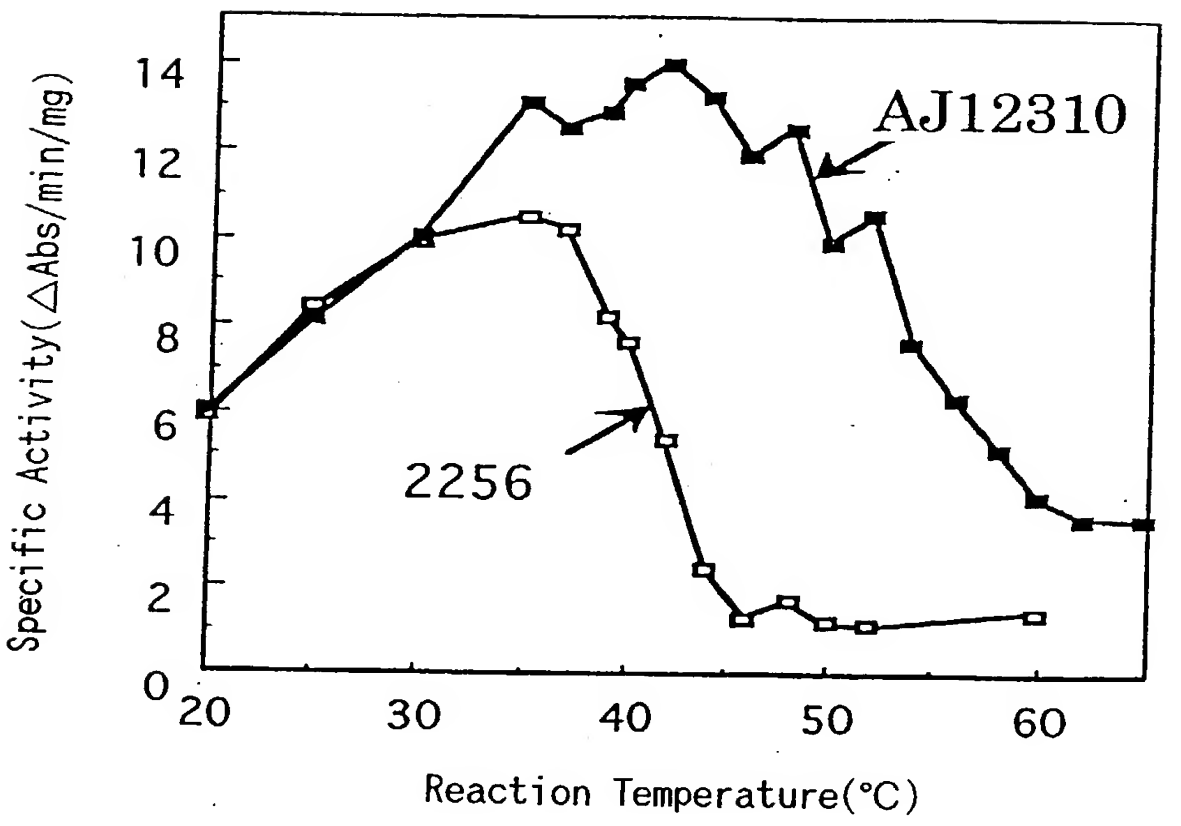


Fig. 1

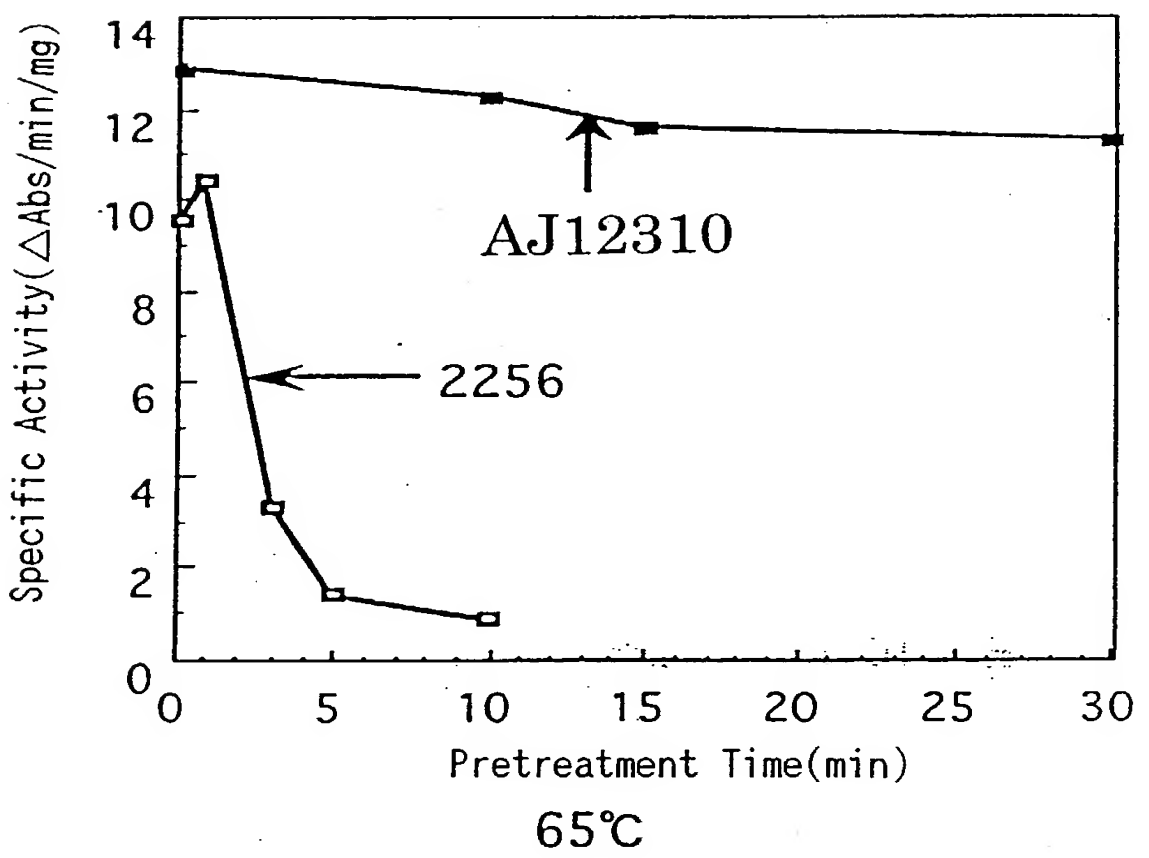
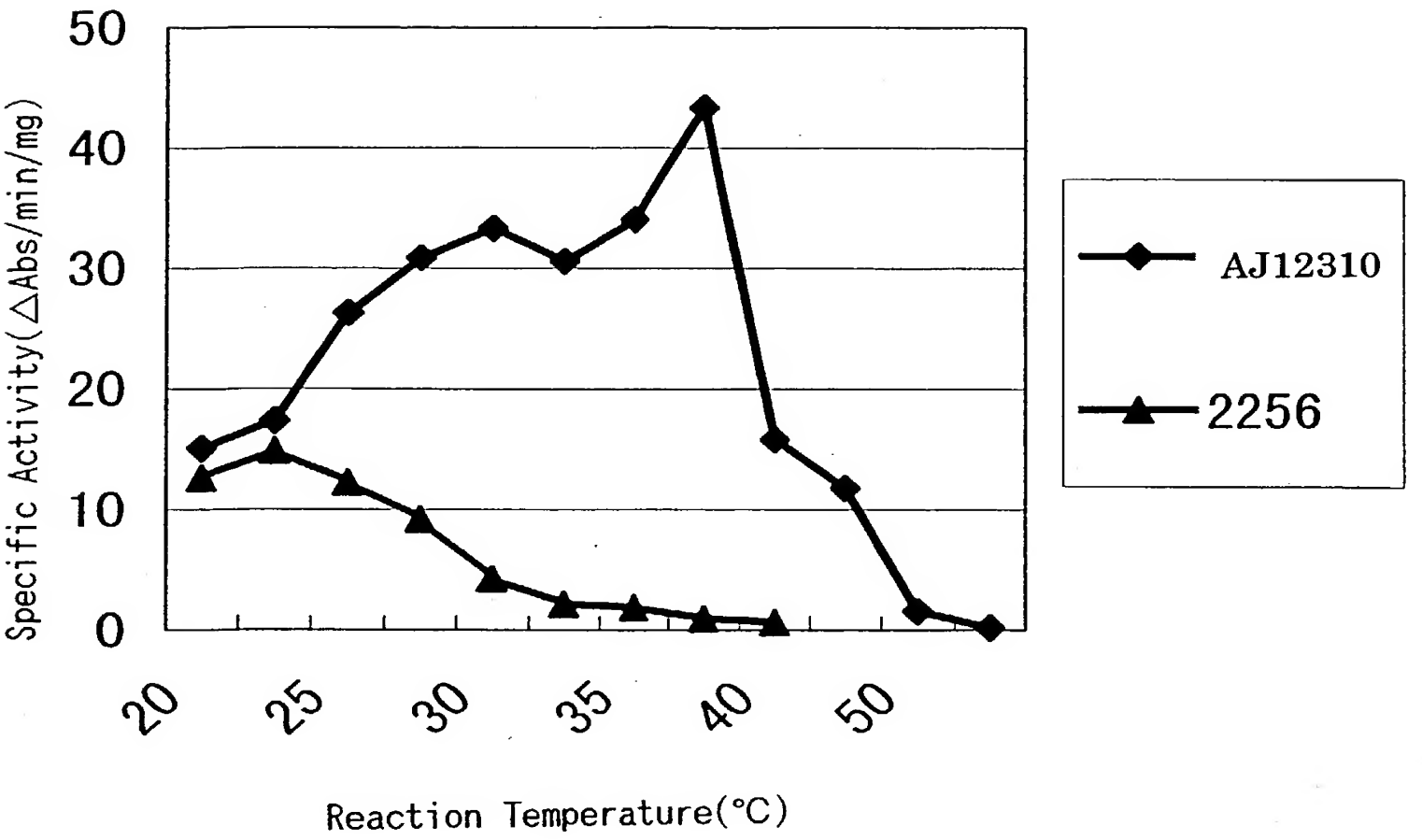


Fig. 2


Specific Activity(△Abs/min/mg)
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40
30
20
10
0
20
25
30
35
40
50
Reaction Temperature(°C)
AJ12310
2256

Fig. 3

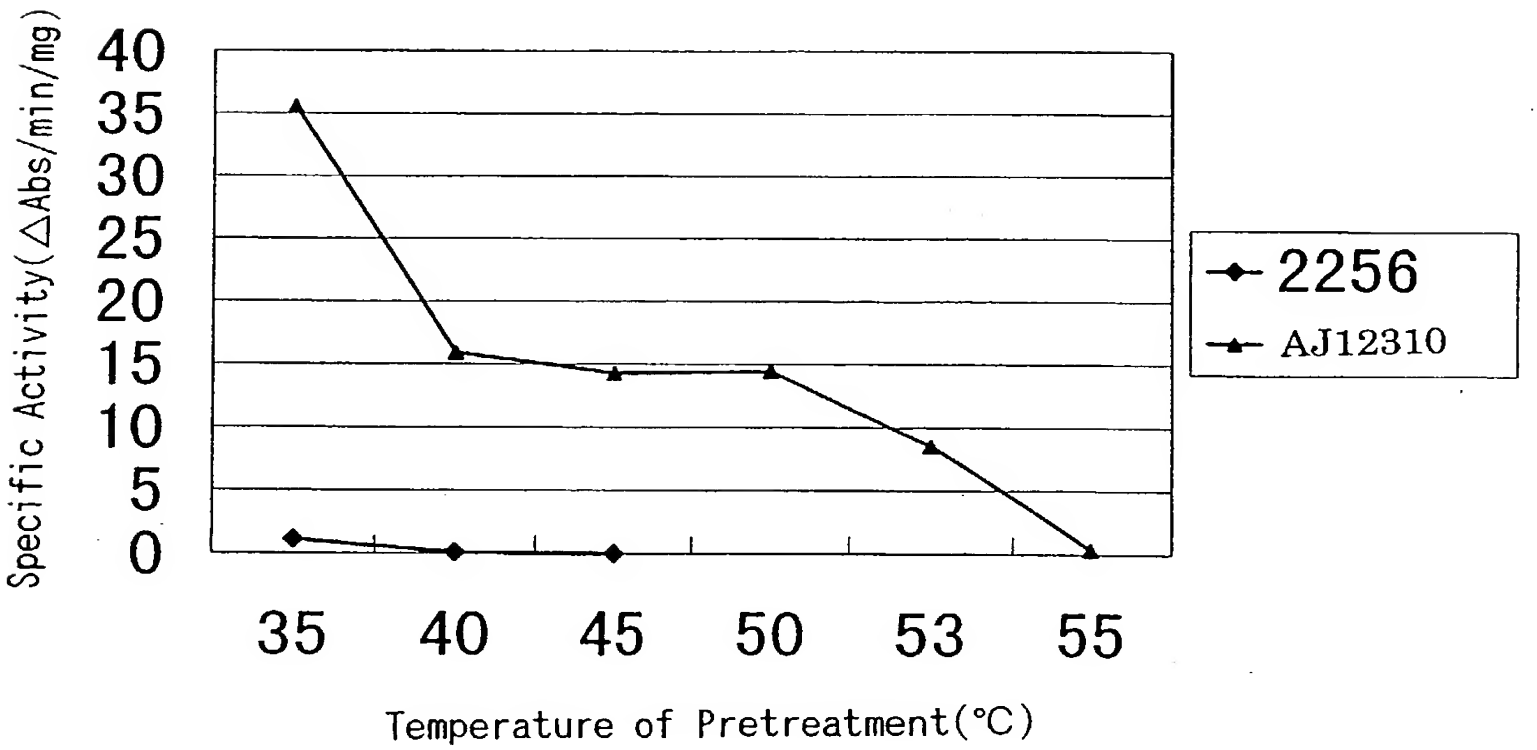
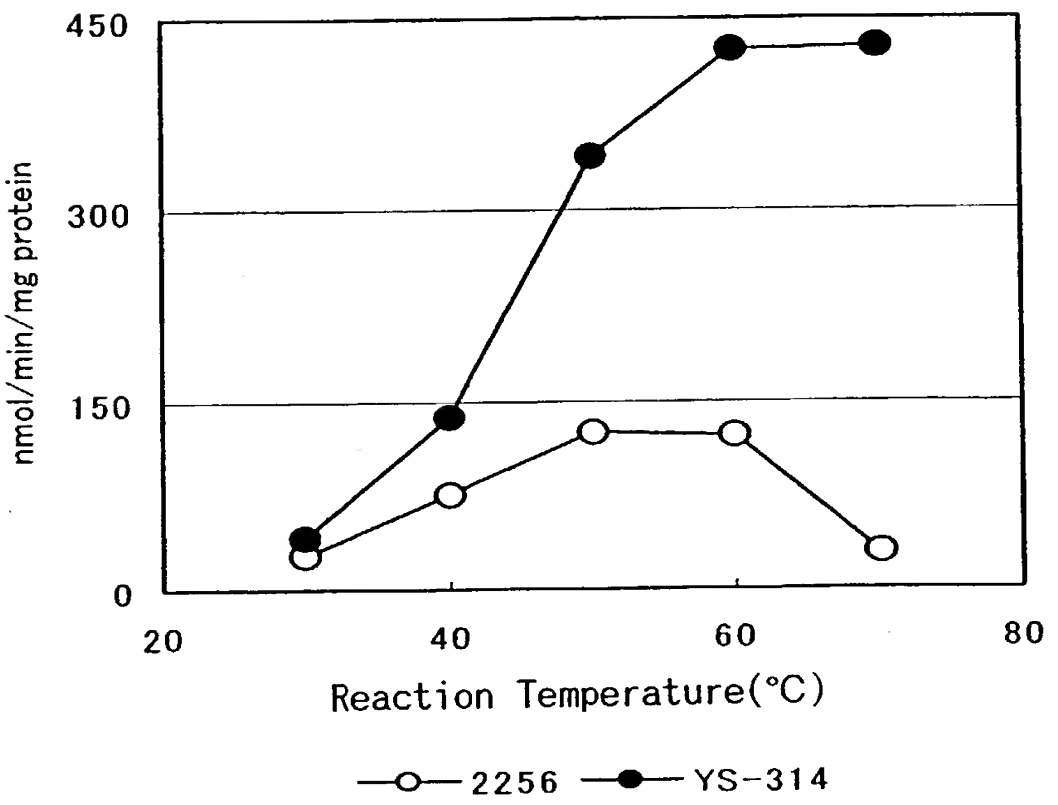

Specific Activity(△Abs/min/mg)
40
35
30
25
20
15
10
5
0
35
40
45
50
53
55
Temperature of Pretreatment(°C)
2256
AJ12310

Fig. 4

Fig. 5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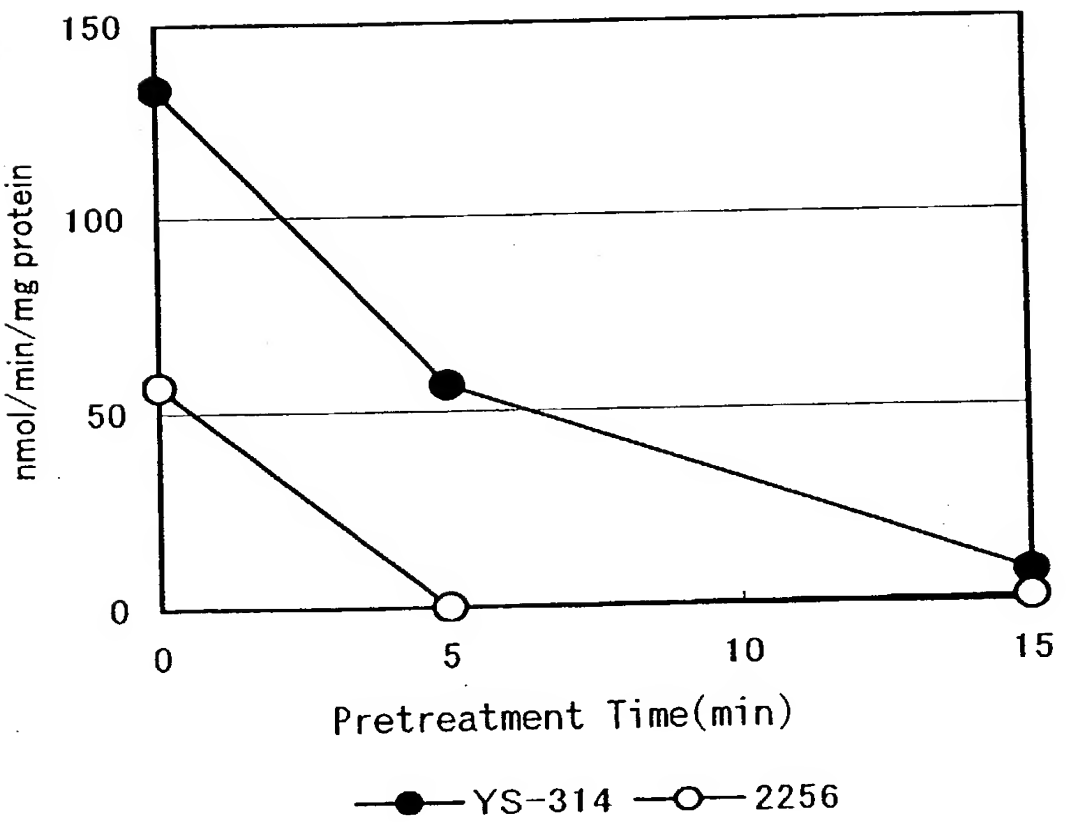
nmol/min/mg protein
20
40
60
80
Reaction Temperature(°C)
2256
YS-314

Fig. 6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100
50
0
nmol/min/mg protein
0
5
10
15
Pretreatment Time(min)
YS-314
2256

Fig. 7

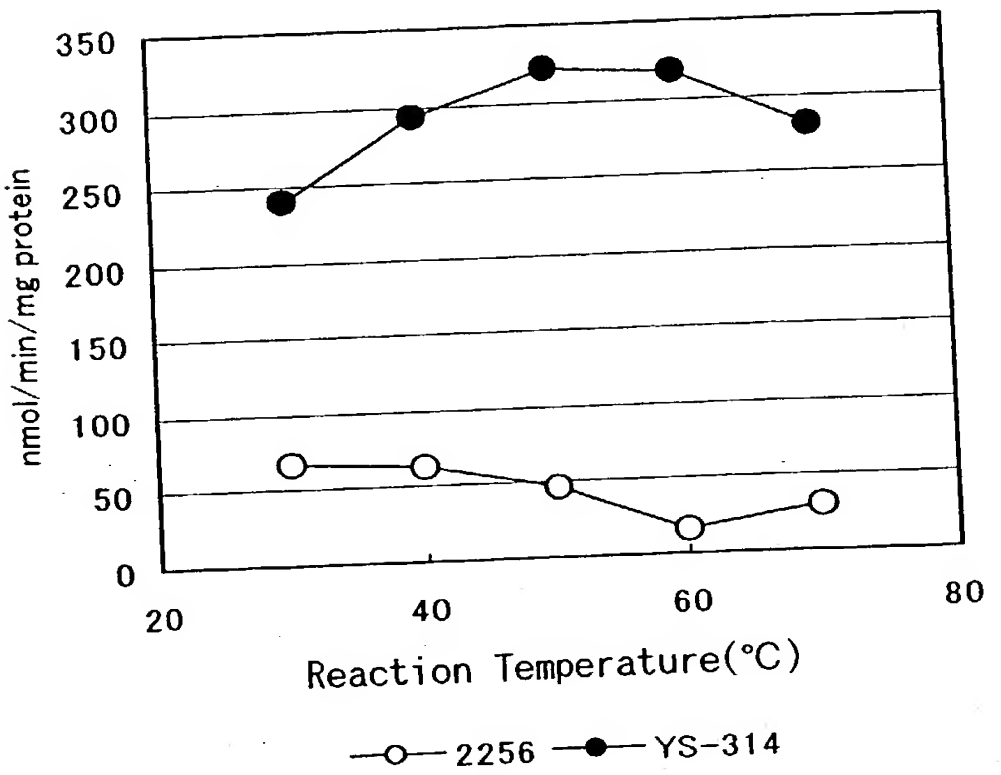


Fig. 8

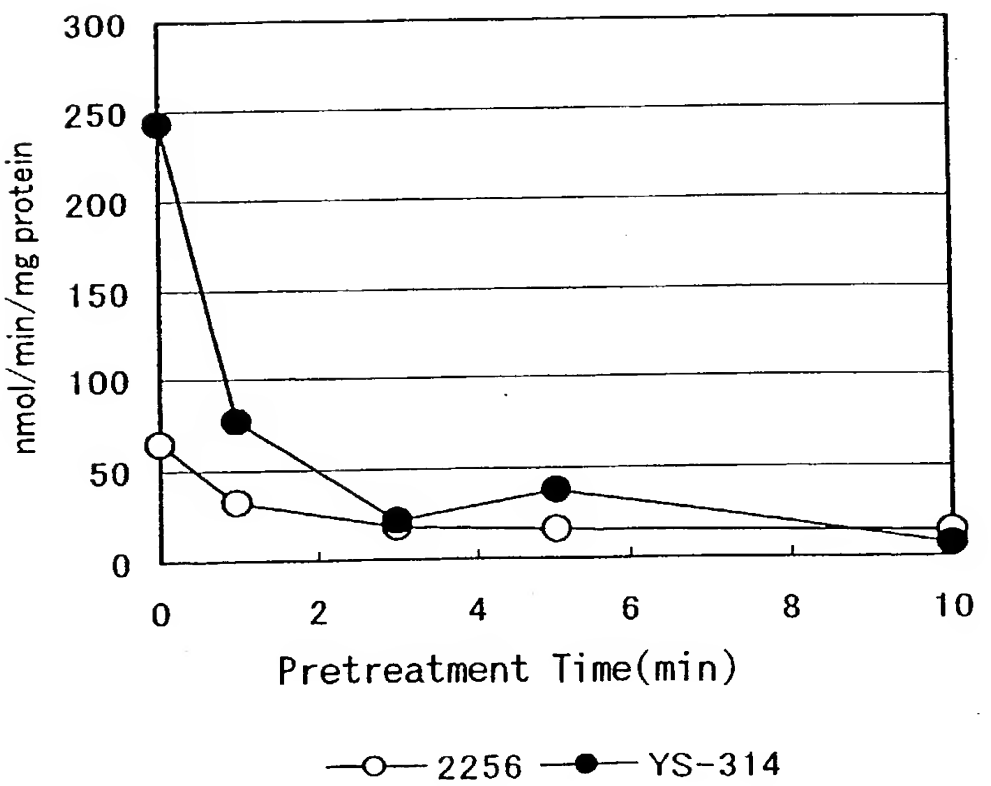


Fig. 9

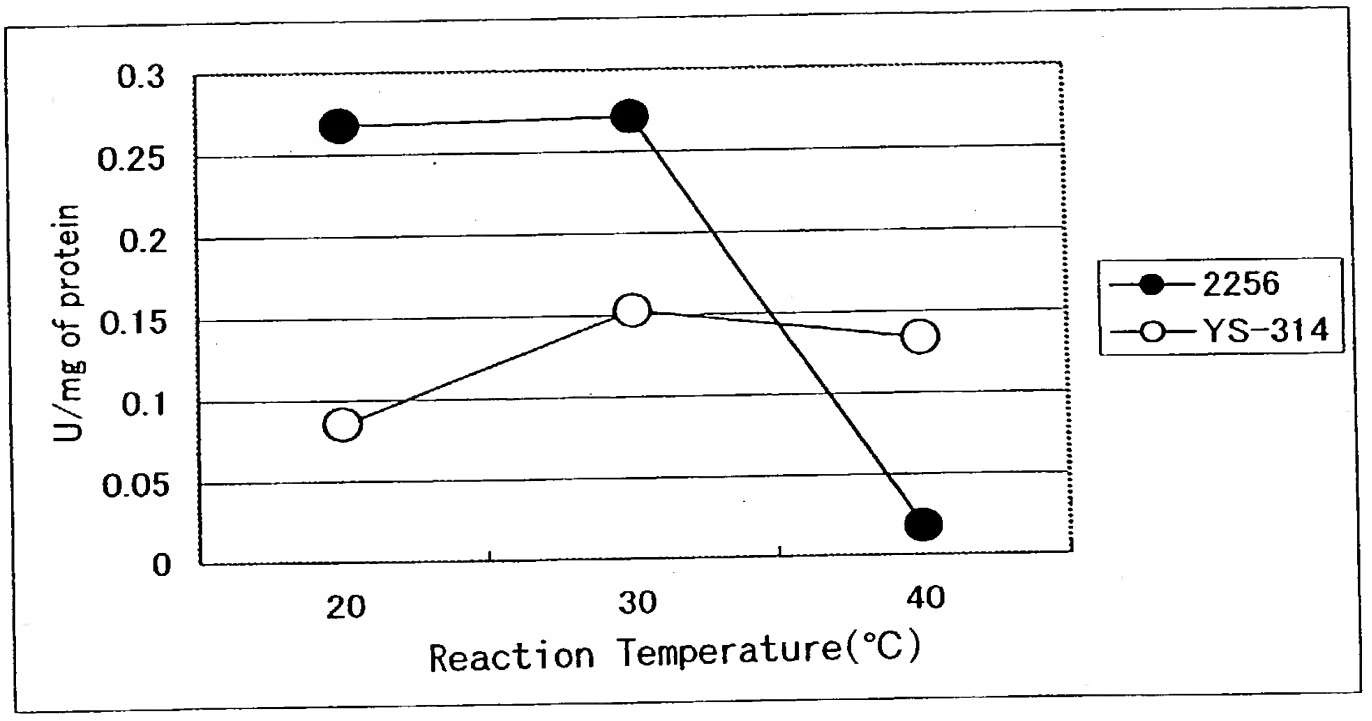

0.3
0.25
0.2
0.15
0.1
0.05
0
U/mg of protein
20
30
40
Reaction Temperature(°C)
2256
YS-314

Fig. 10

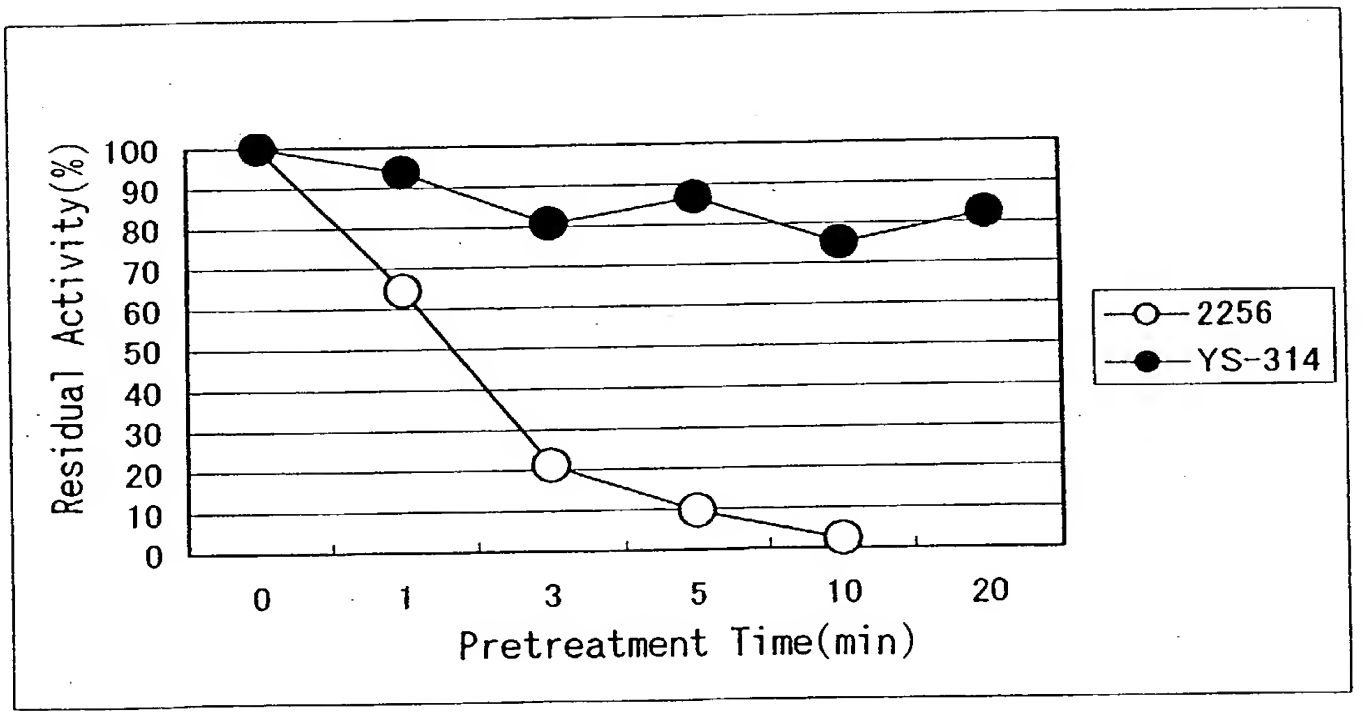

100
90
80
70
60
50
40
30
20
10
0
Residual Activity(%)
0
1
3
5
10
20
Pretreatment Time(min)
2256
YS-314

Fig. 11

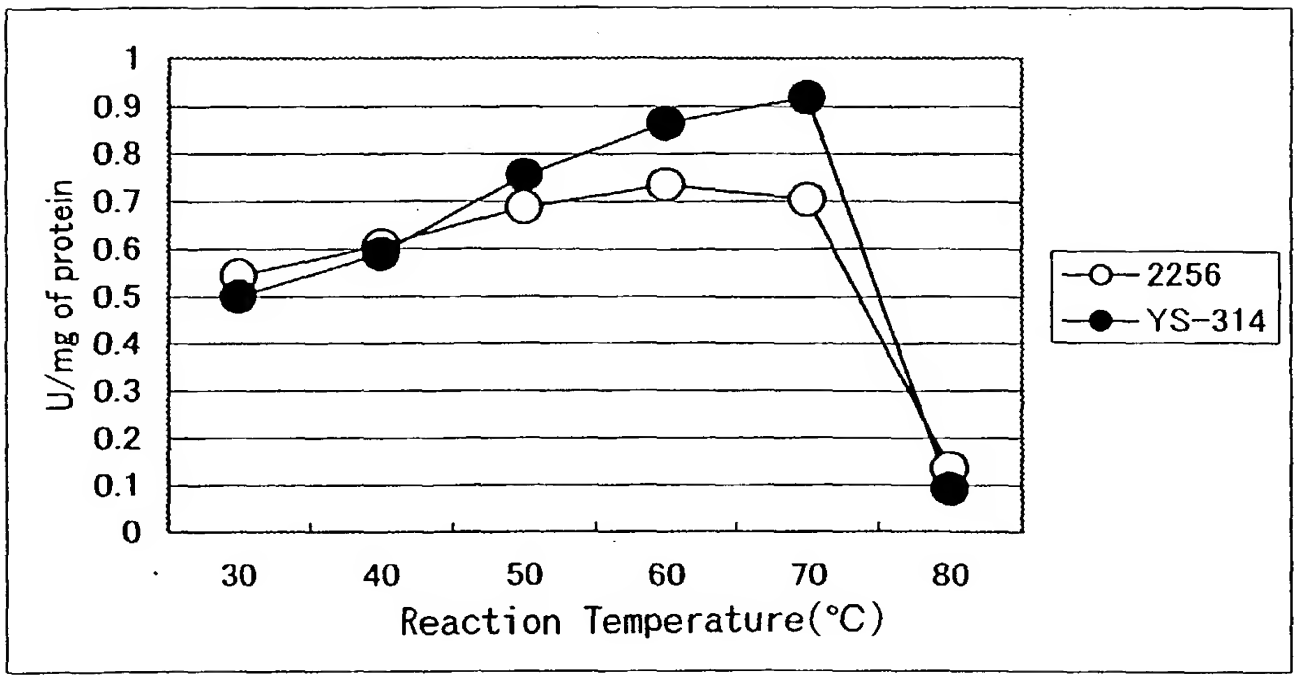


Fig. 12

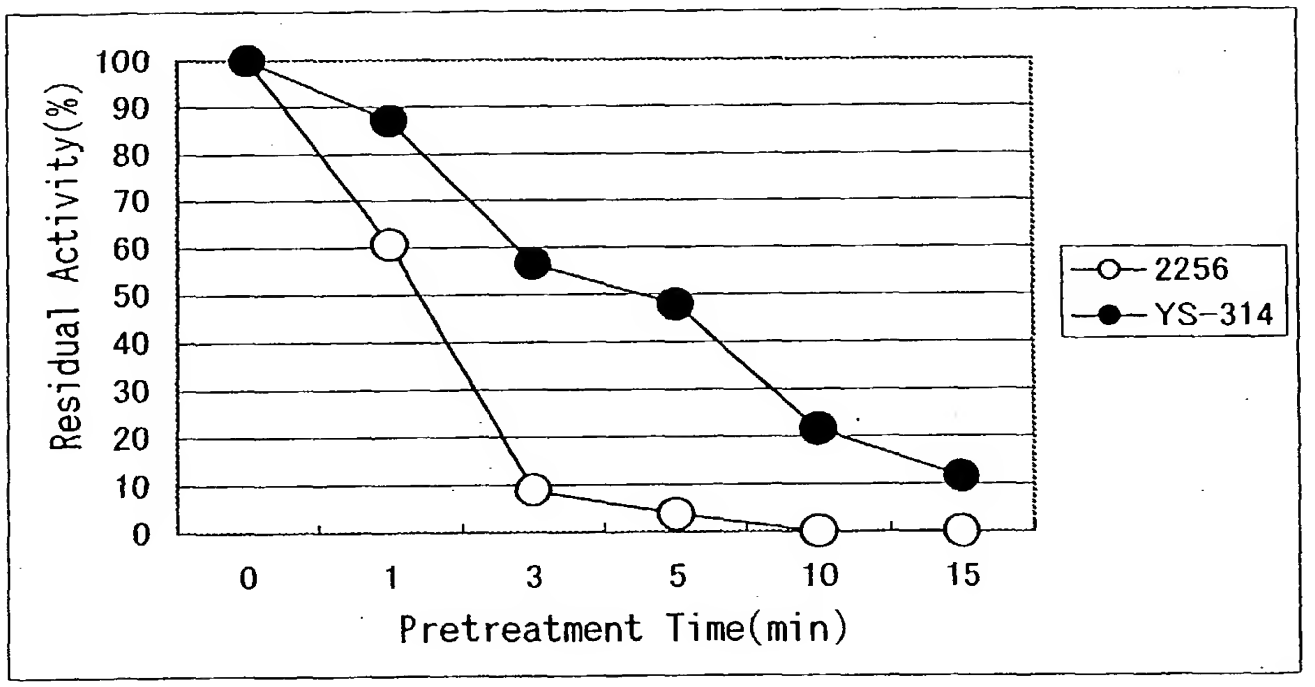


Fig. 13

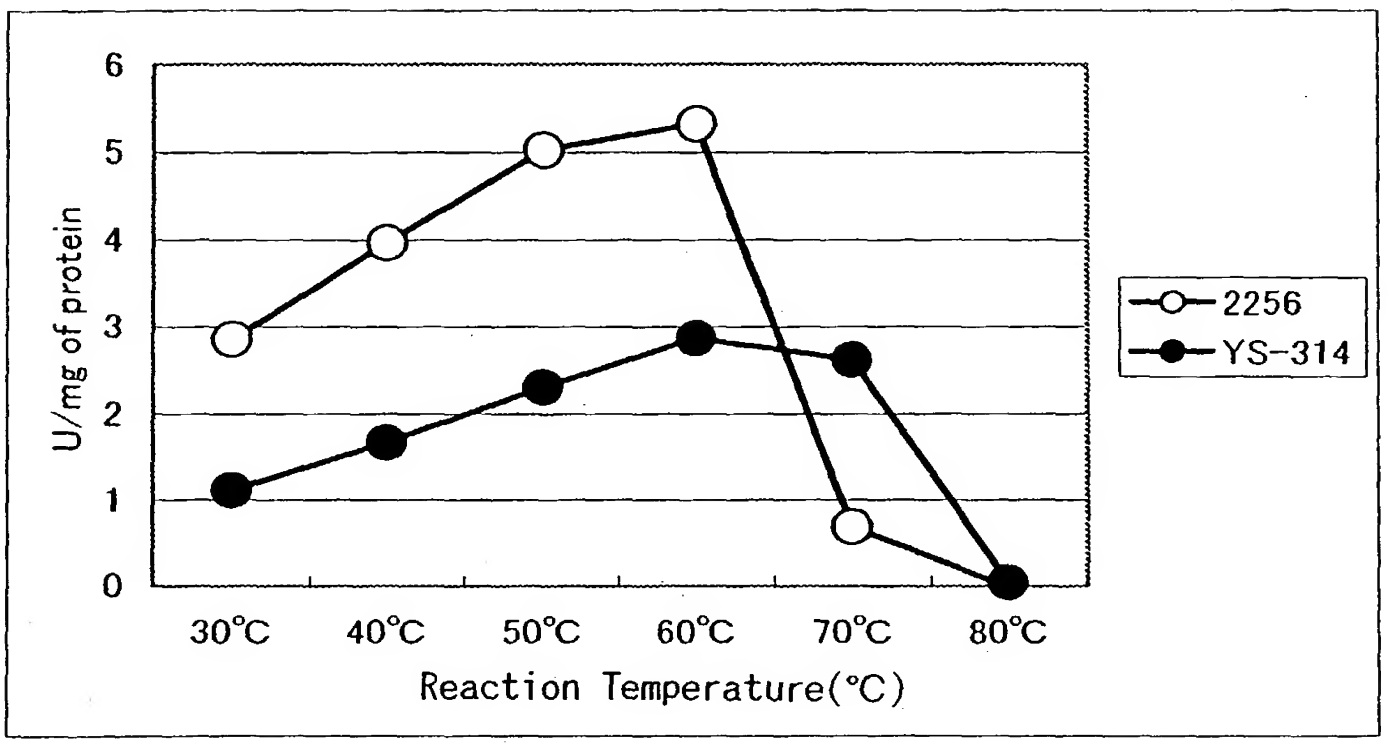
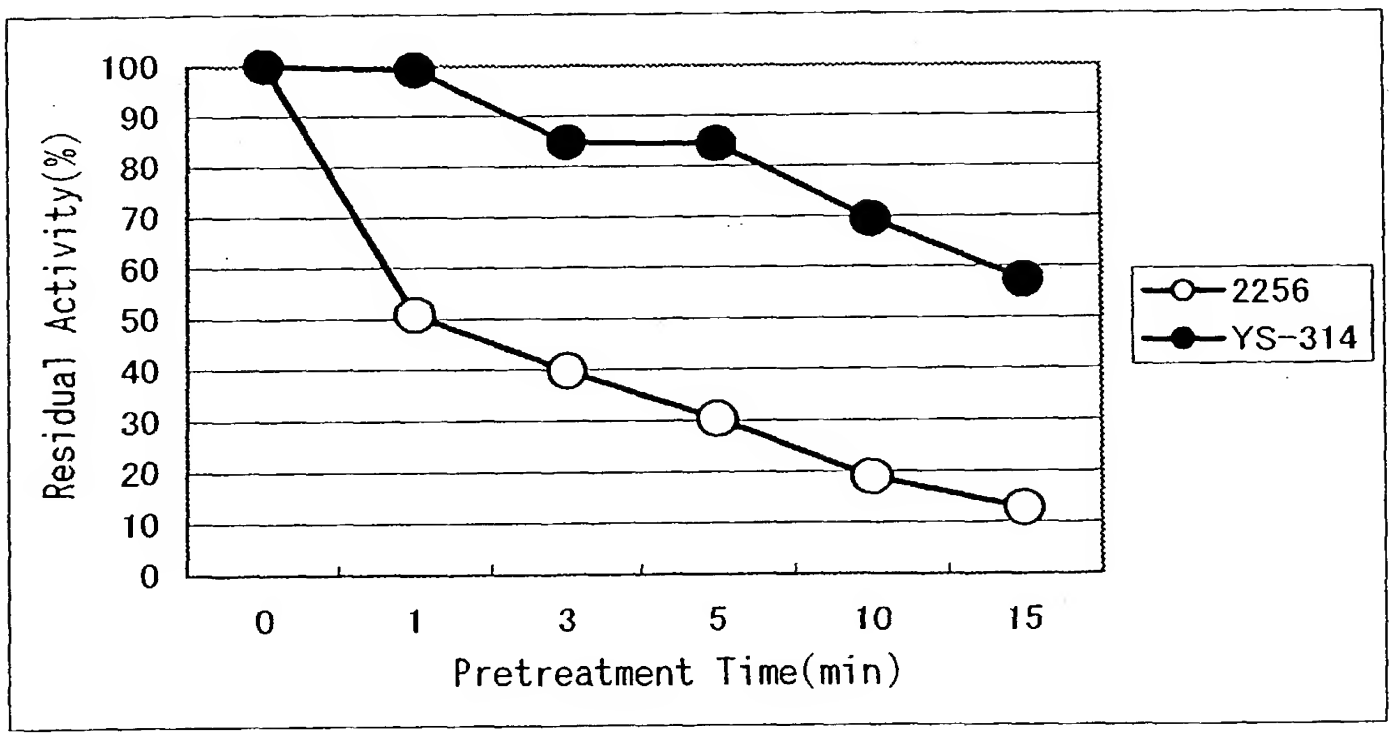


Fig. 14



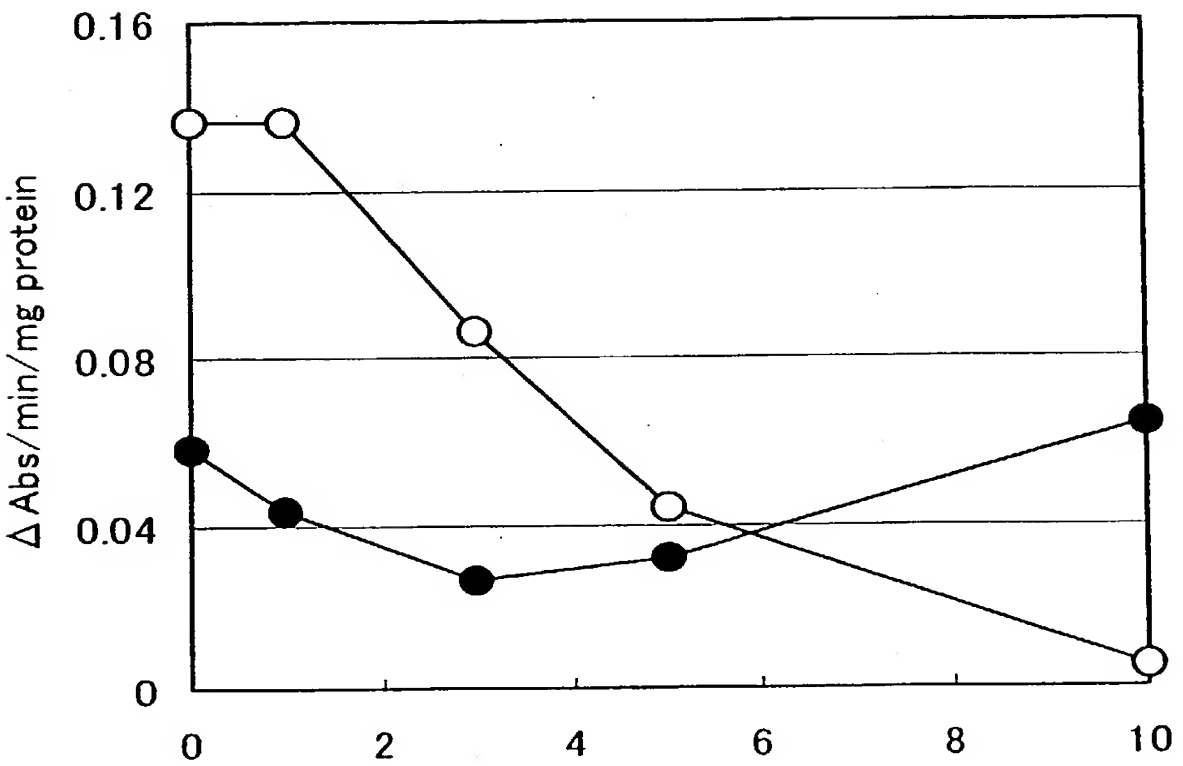

0.16
0.12
0.08
0.04
0
Δ Abs/min/mg protein
0
2
4
6
8
10
Pretreatment Time(min)
2256
YS-314

Fig. 15

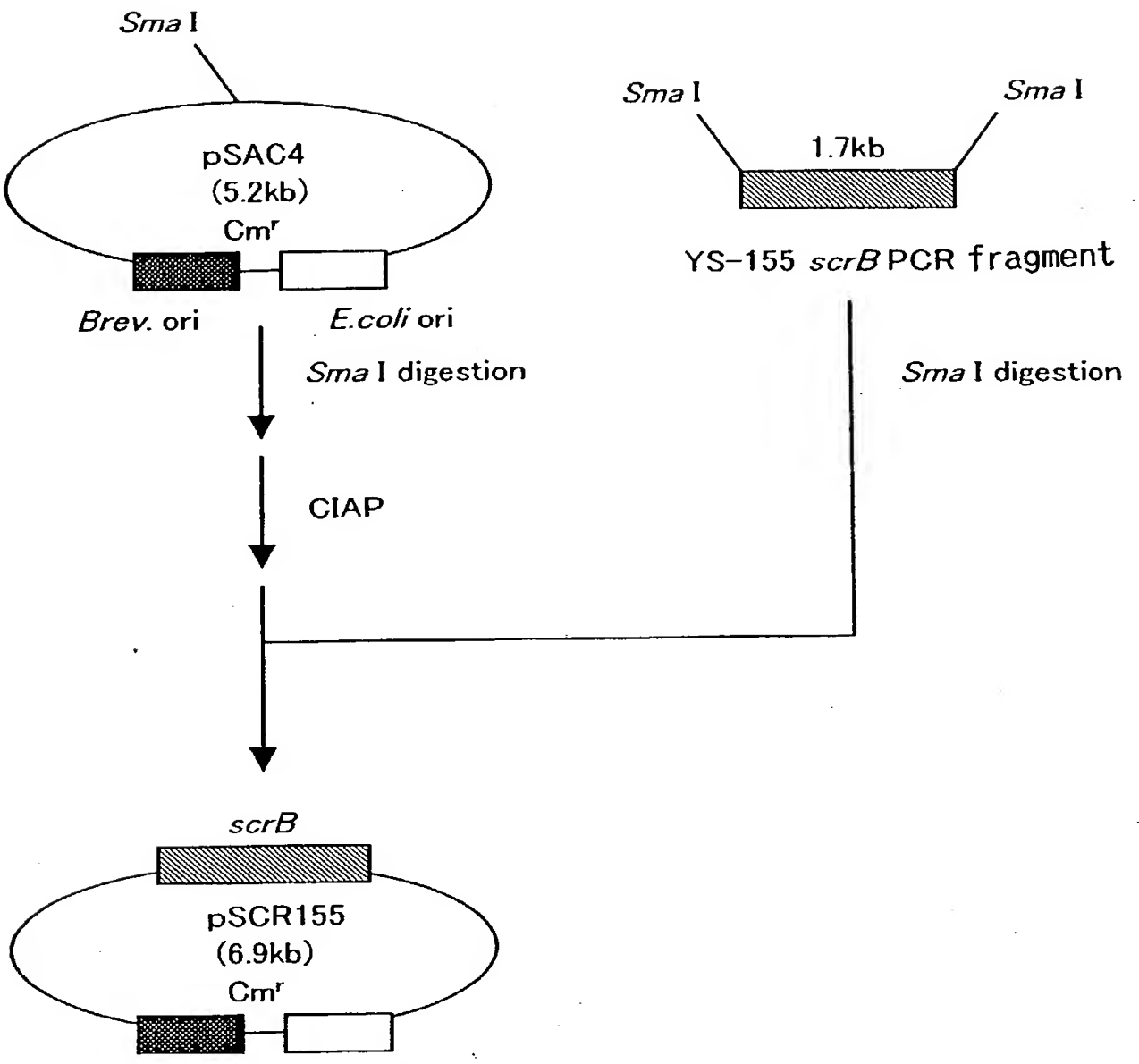
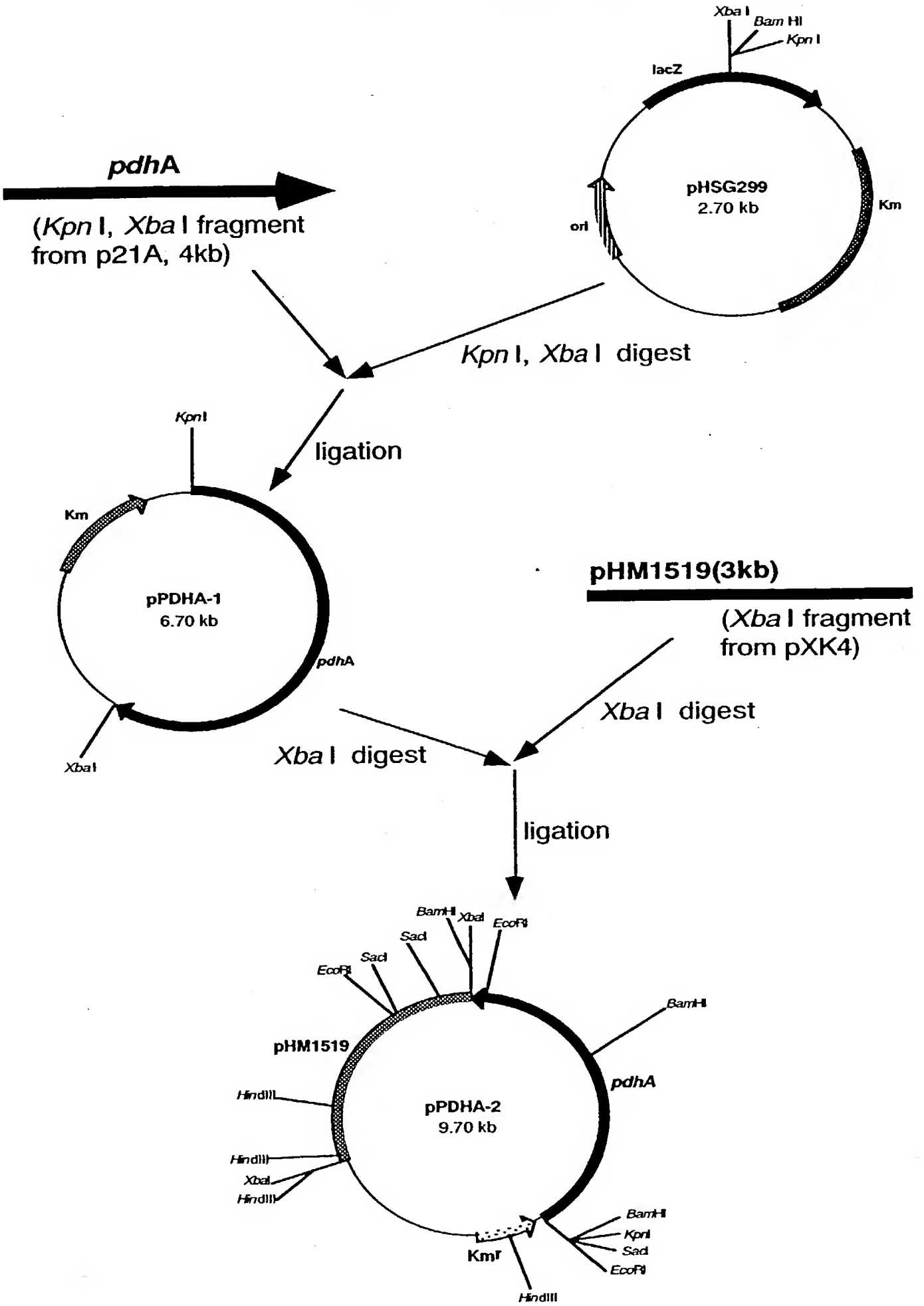


Fig. 16


pdhA
(Kpn I, Xba I fragment
from p21A, 4kb)
Xba I
Bam HI
Kpn I
lacZ
pHSG299
2.70 kb
ori
Km
Kpn I, Xba I digest
ligation
Kpn I
Km
pPDHA-1
6.70 kb
pdhA
Xba I
pHM1519(3kb)
(Xba I fragment
from pXK4)
Xba I digest
Xba I digest
ligation
BamHI
XbaI
EcoRI
SacI
SacI
EcoRI
BamHI
pHM1519
pdhA
HindIII
pPDHA-2
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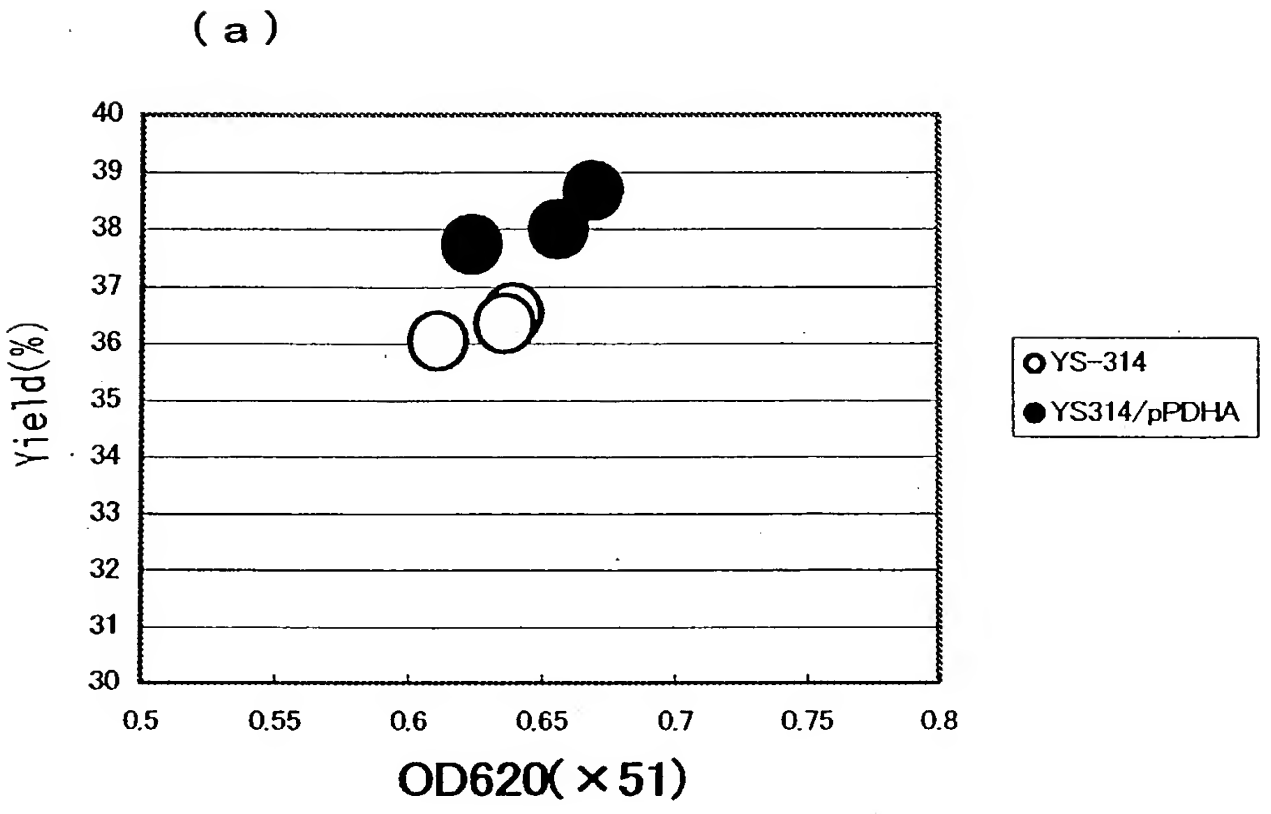
KpnI
SacI
EcoRI
Kmr
HindIII

Fig. 17


(a)
40
39
38
37
36
35
34
33
32
31
30
Yield(%)
0.5
0.55
0.6
0.65
0.7
0.75
0.8
OD620(×51)
YS-314
YS314/pPDHA

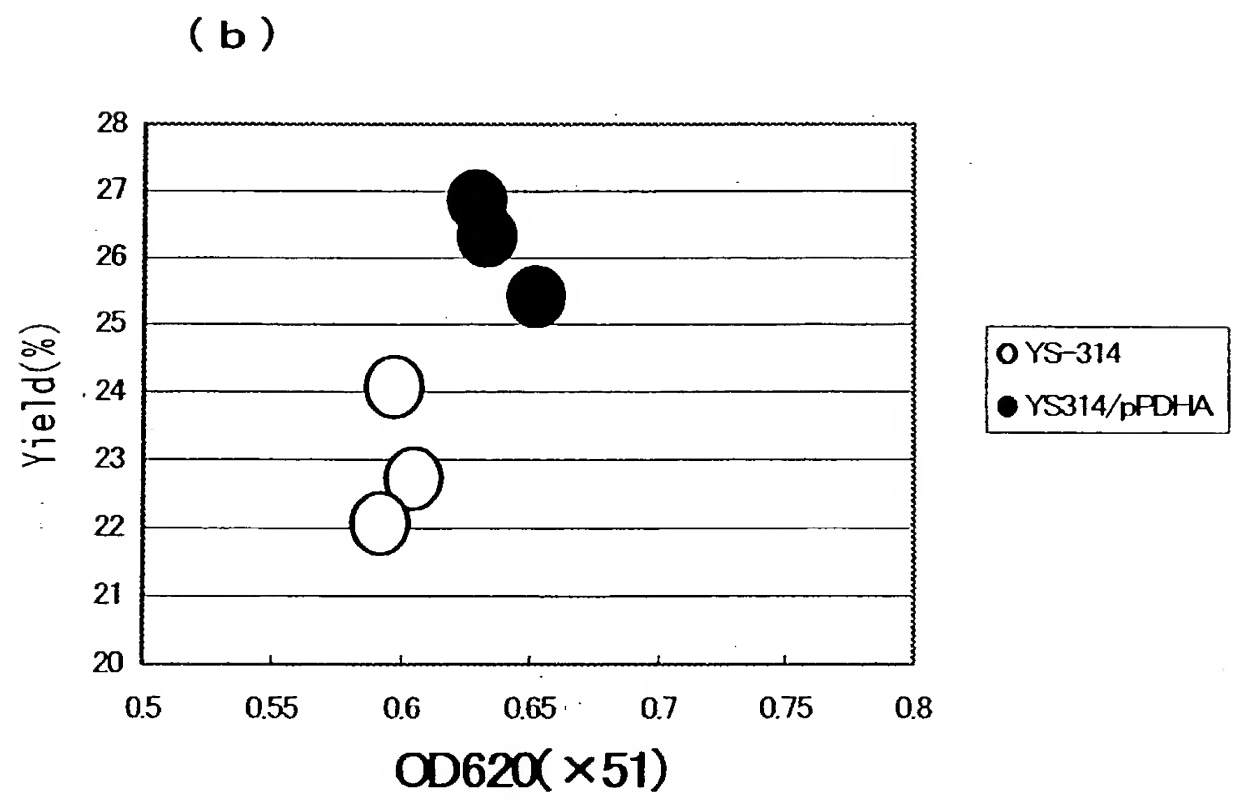
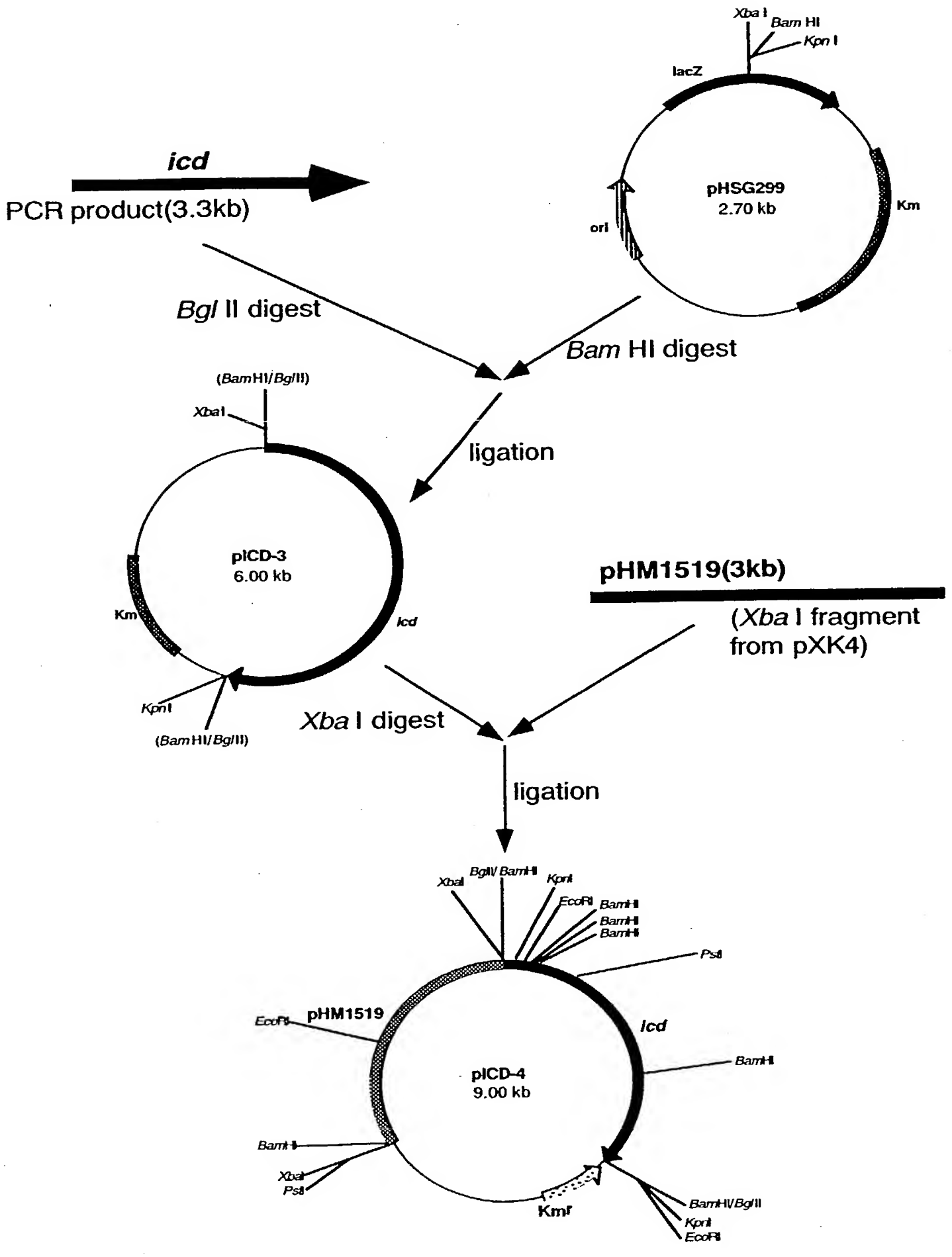

(b)
28
27
26
25
24
23
22
21
20
Yield(%)
0.5
0.55
0.6
0.65
0.7
0.75
0.8
OD620(×51)
YS-314
YS314/pPDHA

Fig. 18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PCR product(3.3kb)
Bgl II digest
Xba I
Bam HI
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ori
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Bam HI digest
ligation
(BamHI/BglII)
XbaI
pICD-3
6.00 kb
Km
icd
KpnI
(BamHI/BglII)
pHM1519(3kb)
(Xba I fragment
from pXK4)
Xba I digest
ligation
XbaI
BglII/ BamHI
KpnI
EcoRI
BamHI
BamHI
BamHI
PstI
EcoRI
pHM1519
icd
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9.00 kb
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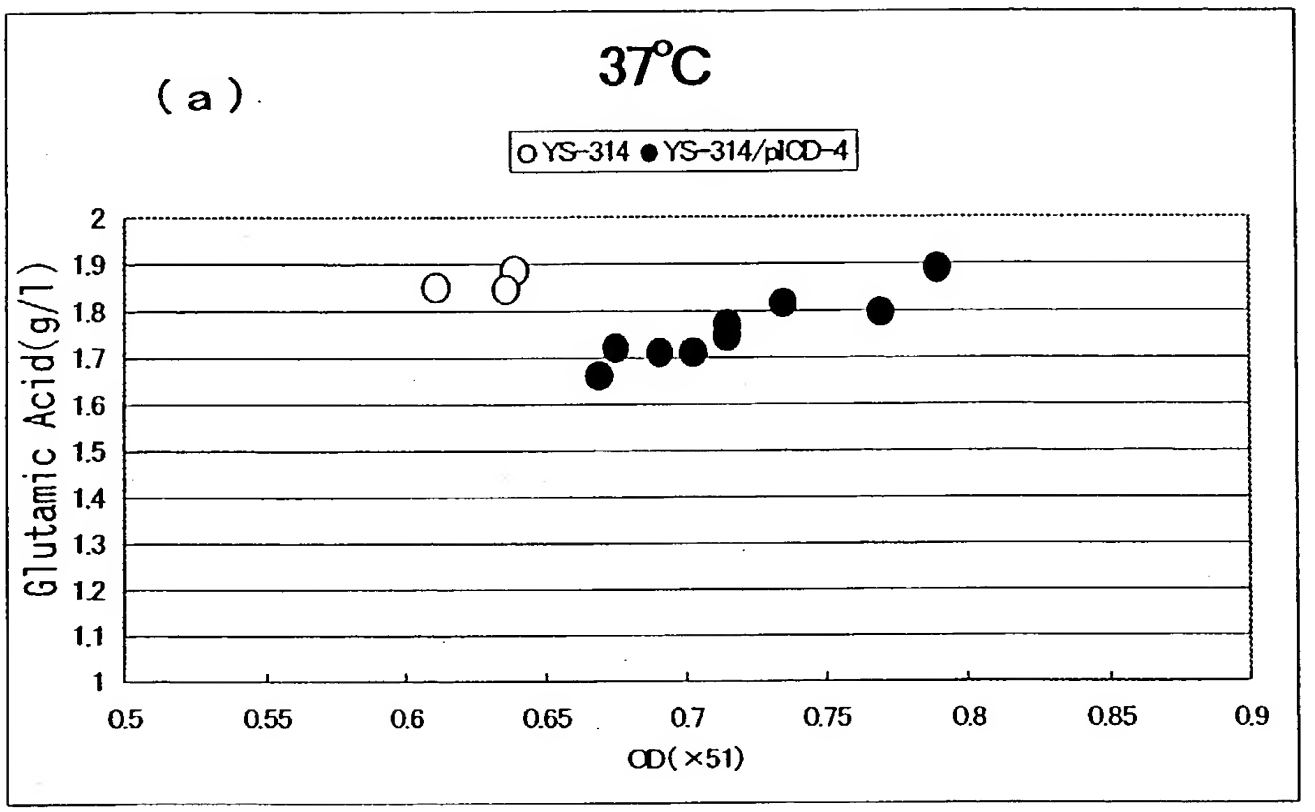
XbaI
PstI
KmR
BamHI/BglII
KpnI
EcoRI

Fig. 19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Glutamic Acid(g/l)
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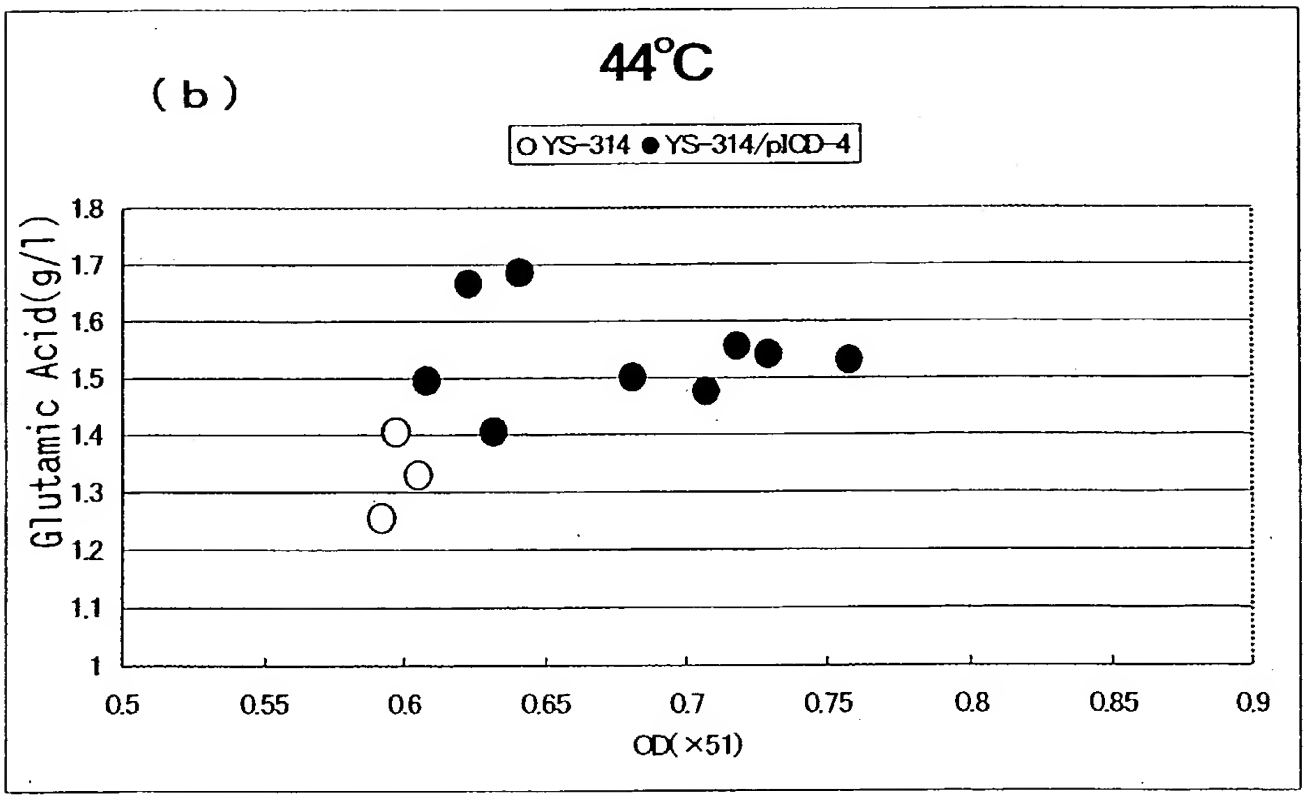
1.8
1.7
1.6
1.5
1.4
1.3
1.2
1.1
1
0.5
0.55
0.6
0.65
0.7
0.75
0.8
0.85
0.9
OD(×51)


(b)
44°C
○YS-314 ●YS-314/pIOD-4
Glutamic Acid(g/l)
1.8
1.7
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1.4
1.3
1.2
1.1
1
0.5
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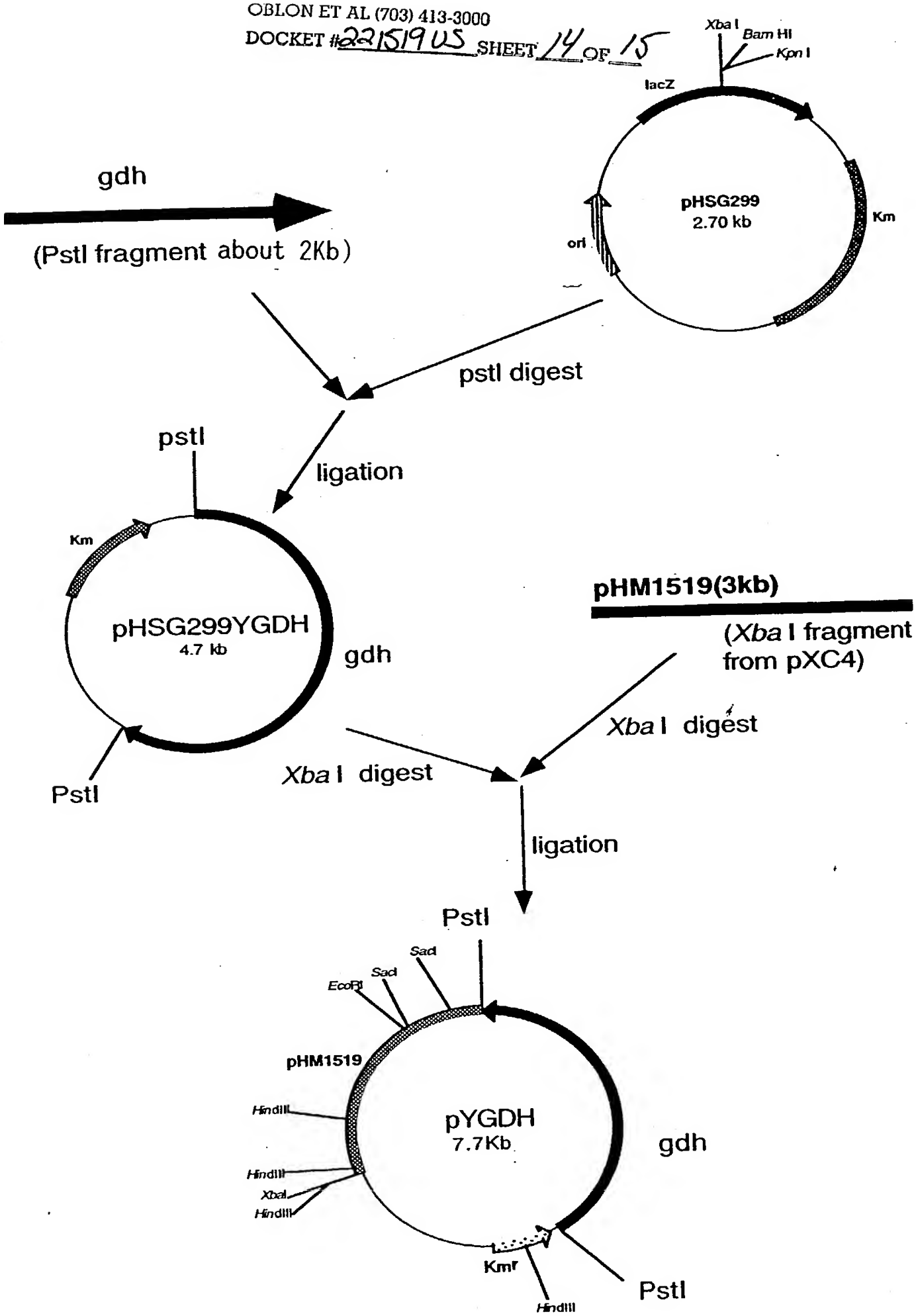
0.6
0.65
0.7
0.75
0.8
0.85
0.9
OD(×51)

Fig. 20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BamHI
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lacZ
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2.70 kb
Km
ori
pstI digest
pstI
ligation
Km
pHSG299YGDH
4.7 kb
gdh
PstI
pHM1519(3kb)
(Xba I fragment
from pXC4)
Xba I digest
Xba I digest
ligation
PstI
SacI
SacI
EcoRI
pHM1519
HindIII
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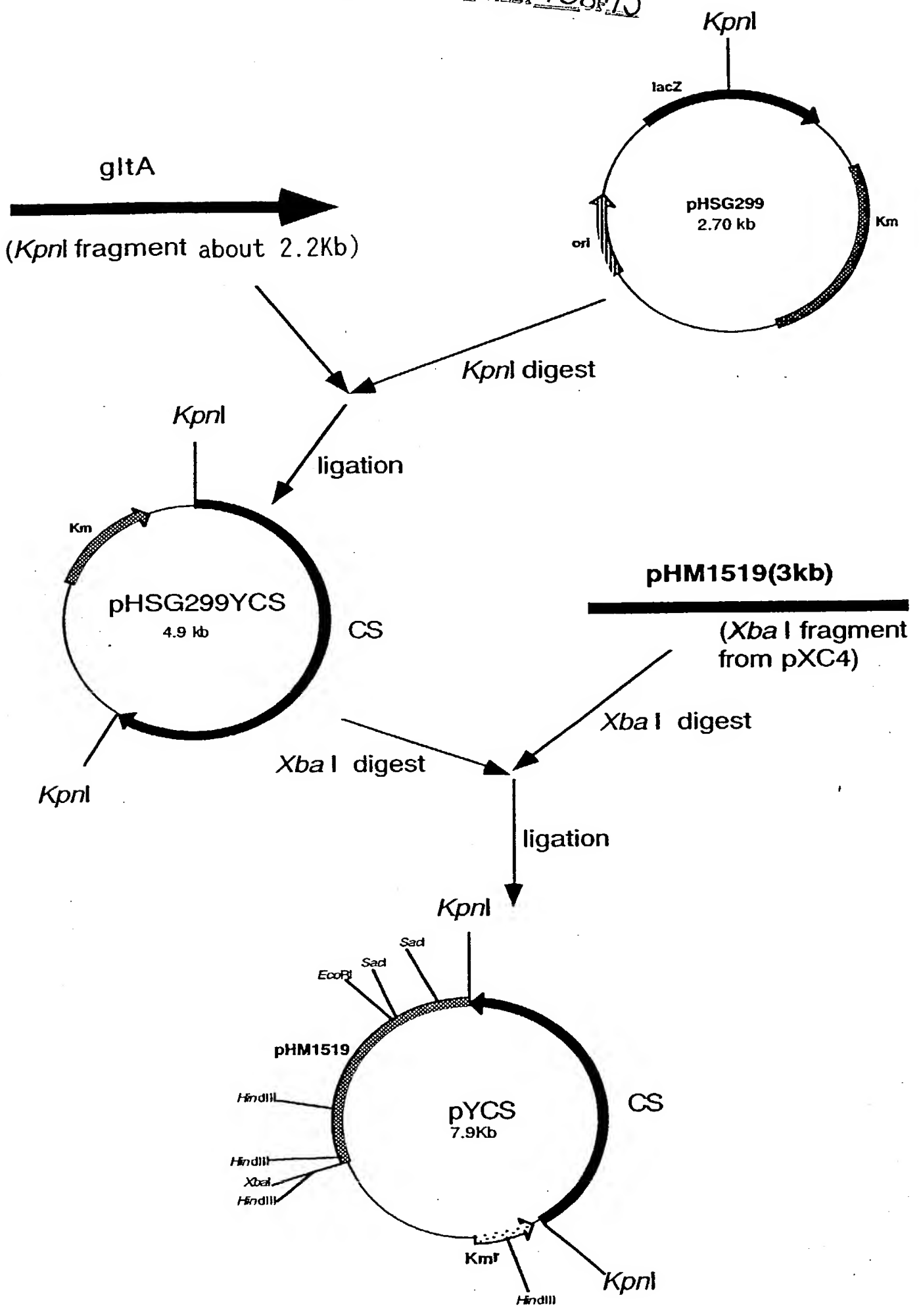
XbaI
HindIII
pYGDH
7.7Kb
gdh
Kmr
HindIII
PstI

Fig. 21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(KpnI fragment about 2.2Kb)
KpnI
lacZ
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2.70 kb
Km
ori
KpnI digest
KpnI
ligation
Km
pHSG299YCS
4.9 kb
CS
pHM1519(3kb)
(Xba I fragment
from pXC4)
Xba I digest
KpnI
Xba I digest
ligation
KpnI
SacI
SacI
EcoRI
pHM1519
HindIII
HindIII
XbaI
HindIII
pYCS
7.9Kb
CS
KmR
KpnI
HindIII

Fig. 22

Declaration, Power Of Attorney and Petition

WE (I) the undersigned inventor(s), hereby declare(s) that:

My residence, post office address and citizenship are as stated below next to my name,

We (I) believe that we are (I am) the original, first, and joint (sole) inventor(s) of the subject matter which is claimed and for which a patent is sought on the invention entitled

GENES FOR HEAT RESISTANT ENZYMES OF AMINO ACID BIOSYNTHETIC PATHWAY DERIVED FROM THERMOPHILIC CORYNEFORM BACTERIA

the specification of which

- ☐ is attached hereto.
- ☐ was filed on _____ as
  Application Serial No. _____
  and amended on _____.
- ☒ was filed as PCT international application
  Number PCT/JP 00/06913
  on October 4, 2000,
  and was amended under PCT Article 19
  on _____ (if applicable).

We (I) hereby state that we (I) have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

We (I) acknowledge the duty to disclose information known to be material to the patentability of this application as defined in Section 1.56 of Title 37 Code of Federal Regulations.

We (I) hereby claim foreign priority benefits under 35 U.S.C. § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed. Prior Foreign Application(s)

Application No.	Country	Day/Month/Year	Priority Claimed
11-282716	Japan	04/10/1999	☒ Yes ☐ No
11-311147	Japan	01/11/1999	☒ Yes ☐ No
2000-120687	Japan	21/04/2000	☒ Yes ☐ No
			☐ Yes ☐ No

We (I) hereby claim the benefit under Title 35, United States Code, § 119(e) of any United States provisional application(s) listed below.

(Application Number)	(Filing Date)
(Application Number)	(Filing Date)

We (I) hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s), or § 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR § 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

Application Serial No.	Filing Date	Status (pending, patented, abandoned)

(24)

And we (I) hereby appoint: Norman F. Oblon, Registration Number 24,618; Marvin J. Spivak, Registration Number 24,913; C. Irvin McClelland, Registration Number 21,124; Gregory J. Maier, Registration Number 25,599; Arthur I. Neustadt, Registration Number 24,854; Richard D. Kelly, Registration Number 27,757; James D. Hamilton, Registration Number 28,421; Eckhard H. Kuesters, Registration Number 28,870; Robert T. Pous, Registration Number 29,099; Charles L. Gholz, Registration Number 26,395; Vincent J. Sunderdick, Registration Number 29,004; William E. Beaumont, Registration Number 30,996; Steven B. Kelber, Registration Number 30,073; Robert F. Gnuse, Registration Number 27,295; Jean-Paul Lavalleye, Registration Number 31,451; Timothy R. Schwartz, Registration Number 32,171; Stephen G. Baxter, Registration Number 32,884; Martin M. Zoltick, Registration Number 35,745; Robert W. Hahl, Registration Number 33,893; Richard L. Treanor, Registration Number 36,379; Steven P. Weihrouch, Registration Number 32,829; John T. Goolkasian, Registration Number 26,142; Marc R. Labgold, Registration Number 34,651; William J. Healey, Registration Number 36,160; and Richard L. Chinn, Registration Number 34,305; our (my) attorneys, with full powers of substitution and revocation, to prosecute this application and to transact all business in the Patent Office connected therewith; and we (I) hereby request that all correspondence regarding this application be sent to the firm of OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT, P.C., whose Post Office Address is: Fourth Floor, 1755 Jefferson Davis Highway, Arlington, Virginia 22202.

We (I) declare that all statements made herein of our (my) own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

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Date

12-00

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Date

NAME OF THIRTEENTH JOINT INVENTOR

Signature of Inventor

Date

SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

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cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cca cgc 642
Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro Arg
10 15 20
tgg aac gga atc acc cgc gac tac acc gct gag cag gta gct gag ctc 690
Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Glu Gln Val Ala Glu Leu
25 30 35
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Gln Gly Ser Val Val Glu Glu His Thr Leu Ala Lys Arg Gly Ala Glu
40 45 50
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Ile Leu Trp Asp Ala Val Ser Ala Glu Gly Asp Asp Tyr Ile Asn Ala
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170 175 180
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Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly Gly
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Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala Arg
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acc gac gca gag gcc gcc acc ctg atc acc tct gat gtt gat gag cgc   1314
Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu Arg
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gac cgc cca ttc atc acc ggc gag cgc acc gcc gag ggc tac tac cac   1362
Asp Arg Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr His
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Val Lys Pro Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr Ala
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Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu Glu
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375                 380                 385                 390
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Thr Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu Lys
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Ala Lys Arg Gly Ala Glu Ile Leu Trp Asp Ala Val Ser Ala Glu Gly
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Asp Asp Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
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Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
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Val Ala Gly Asp Ala Asn Leu Ala Gly His Thr Tyr Pro Asp Gln Ser
100 105 110
Leu Tyr Pro Ala Asn Ser Val Pro Asn Val Val Arg Arg Ile Asn Asn
115 120 125
Ala Leu Leu Arg Ala Asp Glu Ile Ala Arg Val Glu Gly Asp Thr Ser
130 135 140
Val Asp Asn Trp Leu Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
145 150 155 160
Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Gly Met Ile Thr Ala
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Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
180 185 190
Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
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Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
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Ser Asp Val Asp Glu Arg Asp Arg Pro Phe Ile Thr Gly Glu Arg Thr
245 250 255
Ala Glu Gly Tyr Tyr His Val Lys Pro Gly Leu Glu Pro Cys Ile Ala

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Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
275 280 285
Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
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Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
305 310 315 320
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325 330 335
Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
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Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
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Arg Glu Gly Met Pro Ala Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
370 375 380
Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
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Val Phe Arg Ala Ala Arg Asp Glu Gly Ile Ala Ser Val Ala Val Tyr
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Ala Glu Pro Asp Ala Asp Ala Pro Phe Val Glu Tyr Ala Asp Glu Ala
        40                  45                  50
ttc gca ctc ggt ggc cag act tcc gca gag tcc tac ctc gtc att gac                    786
Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu Ser Tyr Leu Val Ile Asp
    55                  60                  65                  70
aag atc att gac gca gca cgc aag tcc ggt gca gac gct gtc cac ccc                    834
Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly Ala Asp Ala Val His Pro
                75                  80                  85
ggc tac ggc ttc ctc gcc gag aac gcc gat ttc gct gaa gct gtc atc                    882
Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp Phe Ala Glu Ala Val Ile
            90                  95                  100
aac gag ggc ctg atc tgg atc gga cca tcc cct gag tcc atc cgt tcc                    930
Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser Pro Glu Ser Ile Arg Ser
        105                 110                 115
ctc ggt gac aag gtc acc gca cgc cac atc gcc aac aac gcc aac gca                    978
Leu Gly Asp Lys Val Thr Ala Arg His Ile Ala Asn Asn Ala Asn Ala
    120                 125                 130
ccg atg gca ccg ggc acc aag gag cct gtc aag gac gcc gct gag gtt                   1026
Pro Met Ala Pro Gly Thr Lys Glu Pro Val Lys Asp Ala Ala Glu Val
135                 140                 145                 150
gtc gcc ttc gcc gag gag ttc ggt ctc ccc atc gcc atc aag gct gcc                   1074
Val Ala Phe Ala Glu Glu Phe Gly Leu Pro Ile Ala Ile Lys Ala Ala
                155                 160                 165
ttc ggt ggc ggc gga cgt ggc atg aag gtc gcc tac gag atg gac gag                   1122
Phe Gly Gly Gly Gly Arg Gly Met Lys Val Ala Tyr Glu Met Asp Glu
            170                 175                 180
gtc gcc gac ctc ttc gaa tcc gcc acc cgt gag gcc acc gcc gcc ttc                   1170
Val Ala Asp Leu Phe Glu Ser Ala Thr Arg Glu Ala Thr Ala Ala Phe
        185                 190                 195
ggt cgt ggt gag tgc ttc gtg gag cgc tac ctg gac aag gcc cgc cac                   1218
Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr Leu Asp Lys Ala Arg His
    200                 205                 210
gtc gag gca cag gtc atc gcc gac aag cac ggc aac gtt gtg gtc gcc                   1266
Val Glu Ala Gln Val Ile Ala Asp Lys His Gly Asn Val Val Val Ala
215                 220                 225                 230
```

```
ggt acc cgt gac tgc tcc ctg cag cgt cgt ttc cag aag ctc gtc gag   1314
Gly Thr Arg Asp Cys Ser Leu Gln Arg Arg Phe Gln Lys Leu Val Glu
                235                 240                 245
gag gca ccg gca ccg ttc ctc acc gat gag cag cgt gac cgc atc cac   1362
Glu Ala Pro Ala Pro Phe Leu Thr Asp Glu Gln Arg Asp Arg Ile His
            250                 255                 260
tcc tcc gcc aag gct atc tgc cgc gag gcc ggt tac tac ggt gcc ggc   1410
Ser Ser Ala Lys Ala Ile Cys Arg Glu Ala Gly Tyr Tyr Gly Ala Gly
        265                 270                 275
acc gtg gag tac ctg gtc ggt tcc gac gga ctg atc tcc ttc ctg gag   1458
Thr Val Glu Tyr Leu Val Gly Ser Asp Gly Leu Ile Ser Phe Leu Glu
    280                 285                 290
gtc aac acc cgc ctg cag gtg gag cac ccc gtc acc gag gag acc acc   1506
Val Asn Thr Arg Leu Gln Val Glu His Pro Val Thr Glu Glu Thr Thr
295                 300                 305                 310
ggc atc gac ctg gtg cgc gag atg ttc cgc atc gcc gag ggc gcc gag   1554
Gly Ile Asp Leu Val Arg Glu Met Phe Arg Ile Ala Glu Gly Ala Glu
                315                 320                 325
ctc tcc atc aag gag gac ccg acc cca cgc ggc cac gcc ttc gag ttc   1602
Leu Ser Ile Lys Glu Asp Pro Thr Pro Arg Gly His Ala Phe Glu Phe
            330                 335                 340
cgc atc aac ggc gag gac gca ggc tcc aac ttc atg ccc gca ccg ggc   1650
Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn Phe Met Pro Ala Pro Gly
        345                 350                 355
aag atc acc cgc tac cgt gag ccc gcc ggc ccg ggt gtc cgc atg gac   1698
Lys Ile Thr Arg Tyr Arg Glu Pro Ala Gly Pro Gly Val Arg Met Asp
    360                 365                 370
tcc ggc gtt gtc gag ggt tcc gag atc tcc ggc cag ttc gac tcc atg   1746
Ser Gly Val Val Glu Gly Ser Glu Ile Ser Gly Gln Phe Asp Ser Met
375                 380                 385                 390
ctg gcc aag ctg atc gtc tgg ggc cag acc cgt gag cag gcc ctg gag   1794
Leu Ala Lys Leu Ile Val Trp Gly Gln Thr Arg Glu Gln Ala Leu Glu
                395                 400                 405
cgt tcc cgt cgt gcg ctc ggc gag tac atc gtc gag ggc atg ccg acc   1842
Arg Ser Arg Arg Ala Leu Gly Glu Tyr Ile Val Glu Gly Met Pro Thr
            410                 415                 420
gtc atc ccg ttc cac tcc cac atc gtc tcc aac ccg gca ttc gtc ggt   1890
Val Ile Pro Phe His Ser His Ile Val Ser Asn Pro Ala Phe Val Gly
        425                 430                 435
gac ggc gag ggc ttc gag gtc tac acc aag tgg atc gag gag gtc tgg   1938
Asp Gly Glu Gly Phe Glu Val Tyr Thr Lys Trp Ile Glu Glu Val Trp
    440                 445                 450
gac aac ccg atc gag ccg ttc gtc gat gca gcc gac ctc gac gac gag   1986
```

```
Asp Asn Pro Ile Glu Pro Phe Val Asp Ala Ala Asp Leu Asp Asp Glu
455                 460                 465                 470
gag aag acc ccg tcg cag aag gtc atc gtc gag atc gac ggc cgc cgc   2034
Glu Lys Thr Pro Ser Gln Lys Val Ile Val Glu Ile Asp Gly Arg Arg
                475                 480                 485
gtc gag gtg gct ctc ccg ggc gac ctc gct ctc ggc ggt ggc gca ggt   2082
Val Glu Val Ala Leu Pro Gly Asp Leu Ala Leu Gly Gly Gly Ala Gly
            490                 495                 500
gcc gcc aag aag aag ccg aag aag cgt cgc gca ggt ggc gcc aag gcc   2130
Ala Ala Lys Lys Lys Pro Lys Lys Arg Arg Ala Gly Gly Ala Lys Ala
        505                 510                 515
ggt gtc tcc ggt gac tcc gtc gca gcc ccg atg cag ggc acc gtc atc   2178
Gly Val Ser Gly Asp Ser Val Ala Ala Pro Met Gln Gly Thr Val Ile
    520                 525                 530
aag gtc aac gtt gag gac ggc gcc gag gtc tcc gag ggt gac acc gtc   2226
Lys Val Asn Val Glu Asp Gly Ala Glu Val Ser Glu Gly Asp Thr Val
535                 540                 545                 550
gtg gtt ctc gag gcc atg aag atg gag aac ccg gtc aag gcc cac aag   2274
Val Val Leu Glu Ala Met Lys Met Glu Asn Pro Val Lys Ala His Lys
                555                 560                 565
tcc ggt acc gtc tcc ggt ctg acc atc gcc gcg ggt gag ggc gtg acc   2322
Ser Gly Thr Val Ser Gly Leu Thr Ile Ala Ala Gly Glu Gly Val Thr
            570                 575                 580
aag ggt cag gtt ctc ctg gag atc aag taatccctic agggaacaga         2369
Lys Gly Gln Val Leu Leu Glu Ile Lys
        585                 590
cagccctgtt ct                                                    2381
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<210> 4
<211> 591
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 4

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Val Ser Val Glu Thr Arg Lys Ile Thr Lys Val Leu Val Ala Asn Arg
  1               5                  10                  15
Gly Glu Ile Ala Ile Arg Val Phe Arg Ala Ala Arg Asp Glu Gly Ile
            20                  25                  30
Ala Ser Val Ala Val Tyr Ala Glu Pro Asp Ala Asp Ala Pro Phe Val
        35                  40                  45
Glu Tyr Ala Asp Glu Ala Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu
    50                  55                  60
Ser Tyr Leu Val Ile Asp Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly
```

65 70 75 80
Ala Asp Ala Val His Pro Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp
85 90 95
Phe Ala Glu Ala Val Ile Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser
100 105 110
Pro Glu Ser Ile Arg Ser Leu Gly Asp Lys Val Thr Ala Arg His Ile
115 120 125
Ala Asn Asn Ala Asn Ala Pro Met Ala Pro Gly Thr Lys Glu Pro Val
130 135 140
Lys Asp Ala Ala Glu Val Val Ala Phe Ala Glu Glu Phe Gly Leu Pro
145 150 155 160
Ile Ala Ile Lys Ala Ala Phe Gly Gly Gly Gly Arg Gly Met Lys Val
165 170 175
Ala Tyr Glu Met Asp Glu Val Ala Asp Leu Phe Glu Ser Ala Thr Arg
180 185 190
Glu Ala Thr Ala Ala Phe Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr
195 200 205
Leu Asp Lys Ala Arg His Val Glu Ala Gln Val Ile Ala Asp Lys His
210 215 220
Gly Asn Val Val Val Ala Gly Thr Arg Asp Cys Ser Leu Gln Arg Arg
225 230 235 240
Phe Gln Lys Leu Val Glu Glu Ala Pro Ala Pro Phe Leu Thr Asp Glu
245 250 255
Gln Arg Asp Arg Ile His Ser Ser Ala Lys Ala Ile Cys Arg Glu Ala
260 265 270
Gly Tyr Tyr Gly Ala Gly Thr Val Glu Tyr Leu Val Gly Ser Asp Gly
275 280 285
Leu Ile Ser Phe Leu Glu Val Asn Thr Arg Leu Gln Val Glu His Pro
290 295 300
Val Thr Glu Glu Thr Thr Gly Ile Asp Leu Val Arg Glu Met Phe Arg
305 310 315 320
Ile Ala Glu Gly Ala Glu Leu Ser Ile Lys Glu Asp Pro Thr Pro Arg
325 330 335
Gly His Ala Phe Glu Phe Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn
340 345 350
Phe Met Pro Ala Pro Gly Lys Ile Thr Arg Tyr Arg Glu Pro Ala Gly
355 360 365
Pro Gly Val Arg Met Asp Ser Gly Val Val Glu Gly Ser Glu Ile Ser
370 375 380
Gly Gln Phe Asp Ser Met Leu Ala Lys Leu Ile Val Trp Gly Gln Thr
385 390 395 400
Arg Glu Gln Ala Leu Glu Arg Ser Arg Arg Ala Leu Gly Glu Tyr Ile
405 410 415

Val Glu Gly Met Pro Thr Val Ile Pro Phe His Ser His Ile Val Ser
420 425 430
Asn Pro Ala Phe Val Gly Asp Gly Glu Gly Phe Glu Val Tyr Thr Lys
435 440 445
Trp Ile Glu Glu Val Trp Asp Asn Pro Ile Glu Pro Phe Val Asp Ala
450 455 460
Ala Asp Leu Asp Asp Glu Glu Lys Thr Pro Ser Gln Lys Val Ile Val
465 470 475 480
Glu Ile Asp Gly Arg Arg Val Glu Val Ala Leu Pro Gly Asp Leu Ala
485 490 495
Leu Gly Gly Gly Ala Gly Ala Ala Lys Lys Lys Pro Lys Lys Arg Arg
500 505 510
Ala Gly Gly Ala Lys Ala Gly Val Ser Gly Asp Ser Val Ala Ala Pro
515 520 525
Met Gln Gly Thr Val Ile Lys Val Asn Val Glu Asp Gly Ala Glu Val
530 535 540
Ser Glu Gly Asp Thr Val Val Val Leu Glu Ala Met Lys Met Glu Asn
545 550 555 560
Pro Val Lys Ala His Lys Ser Gly Thr Val Ser Gly Leu Thr Ile Ala
565 570 575
Ala Gly Glu Gly Val Thr Lys Gly Gln Val Leu Leu Glu Ile Lys
580 585 590

<210> 5
<211> 2128
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (339)..(1967)

<400> 5
gctgtcattc cgaccacatt cgccccggga tccgggctcc accacctccc ggacccatgc 60
cccatacctg cggaaaccac gggaaacacg ggaaaaaccg atctcattca gaccggcggg 120
atccacctgt ggaacagtca gcggcgcggc catggagggc agcgacaggt gacgtccgag 180
cacccggttc cccaccgtgg acacggcatt gatccgacac ggtggggata gtttcatgct 240
gaaaaactat cgctgtgcag ggaggatccg gaatgtgacc tatttcatgg agaaatgatt 300
gtggacgata ccccccgggta cggctaccat tccaaaac atg acc att tcc tca cct 356
Met Thr Ile Ser Ser Pro
1 5
ttg att gac gtc gct aac ctg cca gac atc aac acc acc gcc ggc aag 404
Leu Ile Asp Val Ala Asn Leu Pro Asp Ile Asn Thr Thr Ala Gly Lys

```
                10                  15                  20
atc gcc gac ctg aag gcc cgc cgg gcg gaa gcc cac ttc ccc atg ggt   452
Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pro Met Gly
            25                  30                  35
gaa aag gcc gta gag aag gtc cac gcg gcc aac cgc ctc acc gcg cgc   500
Glu Lys Ala Val Glu Lys Val His Ala Ala Asn Arg Leu Thr Ala Arg
        40                  45                  50
gaa cga ctt gac tac ctg ctc gat gaa ggc tcc ttc atc gaa acc gat   548
Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr Asp
    55                  60                  65                  70
cag ctc gca cgc cac cgc acc acc gcg ttc ggc ctg ggc aac aag cga   596
Gln Leu Ala Arg His Arg Thr Thr Ala Phe Gly Leu Gly Asn Lys Arg
                75                  80                  85
ccg gcc acc gac ggc atc gtc acc ggc tgg ggc acc atc gac ggc cgc   644
Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly Arg
            90                  95                  100
gag gtc tgc atc ttc tcc cag gac ggc acc gtc ttc ggt ggc gca ctc   692
Glu Val Cys Ile Phe Ser Gln Asp Gly Thr Val Phe Gly Gly Ala Leu
        105                 110                 115
ggt gag gtc tac ggc gag aag atg atc aag atc atg gag ctg gcc atc   740
Gly Glu Val Tyr Gly Glu Lys Met Ile Lys Ile Met Glu Leu Ala Ile
    120                 125                 130
gac acc ggc cgc cca ctc atc ggc ctg tac gag ggt gca ggt gcc cgc   788
Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr Glu Gly Ala Gly Ala Arg
135                 140                 145                 150
atc cag gac ggt gcg gtc tcc ctc gac ttc atc tcc cag acc ttc tat   836
Ile Gln Asp Gly Ala Val Ser Leu Asp Phe Ile Ser Gln Thr Phe Tyr
                155                 160                 165
cag aac atc cag gcc tcc ggc gtg atc ccg cag atc tcc gtg atc atg   884
Gln Asn Ile Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Val Ile Met
            170                 175                 180
ggt gcc tgc gcc ggt ggc aac gcc tac ggc ccg gcc ctg acc gac ttc   932
Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly Pro Ala Leu Thr Asp Phe
        185                 190                 195
gtg gtc atg gtg gac aag acc tcg aag atg ttc gtc acc ggc ccc gat   980
Val Val Met Val Asp Lys Thr Ser Lys Met Phe Val Thr Gly Pro Asp
    200                 205                 210
gtg atc aag acc gtc acc ggc gag gag atc acc cag gag gag ctc ggc   1028
Val Ile Lys Thr Val Thr Gly Glu Glu Ile Thr Gln Glu Glu Leu Gly
215                 220                 225                 230
gga gca acc acc cac atg gtc acc gcc ggc aac tcc cac tac acc gtc   1076
Gly Ala Thr Thr His Met Val Thr Ala Gly Asn Ser His Tyr Thr Val
                235                 240                 245
```

```
gcc acc gat gag gag gcc ctc gac tgg gtc cag gac ctc atc tcc ttc   1124
Ala Thr Asp Glu Glu Ala Leu Asp Trp Val Gln Asp Leu Ile Ser Phe
            250                 255                 260
ctg ccc tcc aac aat cgc tcc tac gcc ccg gtg gag gag ttc gac gag   1172
Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro Val Glu Glu Phe Asp Glu
        265                 270                 275
gag gac ggt ggc atc gcc gag aac atc acc gcc gat gac ctg aag ctg   1220
Glu Asp Gly Gly Ile Ala Glu Asn Ile Thr Ala Asp Asp Leu Lys Leu
    280                 285                 290
gat gag atc atc ccg gat tcc gcc acc gtg ccc tat gat gtc cgc gac   1268
Asp Glu Ile Ile Pro Asp Ser Ala Thr Val Pro Tyr Asp Val Arg Asp
295                 300                 305                 310
gtc atc cag tgc ctg acc gac gac ggt gag tac ctg gag atc cag gcc   1316
Val Ile Gln Cys Leu Thr Asp Asp Gly Glu Tyr Leu Glu Ile Gln Ala
                315                 320                 325
gac cga gcc gag aat gtc gtc atc gcc ttc ggc cgc atc gag ggc cag   1364
Asp Arg Ala Glu Asn Val Val Ile Ala Phe Gly Arg Ile Glu Gly Gln
            330                 335                 340
tcc gtc ggt ttc gtc gcc aac cag ccg acc cag ttc gcc ggc tgc ctg   1412
Ser Val Gly Phe Val Ala Asn Gln Pro Thr Gln Phe Ala Gly Cys Leu
        345                 350                 355
gac atc gac tcc tcc gag aag gca gcc cgc ttc gtc cgc acc tgc gat   1460
Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg Phe Val Arg Thr Cys Asp
    360                 365                 370
gcc ttc aac atc ccg atc gtc atg ctt gtc gac gtc ccc ggc ttc ctc   1508
Ala Phe Asn Ile Pro Ile Val Met Leu Val Asp Val Pro Gly Phe Leu
375                 380                 385                 390
ccc ggt gcc ggc cag gag tac ggc ggc atc ctg cgt cgt ggc gcc aaa   1556
Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile Leu Arg Arg Gly Ala Lys
                395                 400                 405
ctg ctc tac gcc tac ggt gag gcc acc gtc ccg aag atc acc gtg acc   1604
Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val Pro Lys Ile Thr Val Thr
            410                 415                 420
atg cgc aag gcc tac ggc ggt gcg tac tgt gtc atg gga tcc aag ggt   1652
Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Gly
        425                 430                 435
ctg ggc gca gac atc aac ctg gcc tgg ccg acc gcg cag atc gcc gtc   1700
Leu Gly Ala Asp Ile Asn Leu Ala Trp Pro Thr Ala Gln Ile Ala Val
    440                 445                 450
atg ggt gcc gcc ggc gcg gtc cag ttc atc tac cgc aag gag ctc atg   1748
Met Gly Ala Ala Gly Ala Val Gln Phe Ile Tyr Arg Lys Glu Leu Met
455                 460                 465                 470
gcc gct gat gcc aag ggc ctg gac acc gtc gcc ctg gcc cag tcc ttc   1796
```

```
Ala Ala Asp Ala Lys Gly Leu Asp Thr Val Ala Leu Ala Gln Ser Phe
                475                 480                 485
gag cgt gag tac gag gac cac atg ctc aac ccg tac ctg gcg gcc gag   1844
Glu Arg Glu Tyr Glu Asp His Met Leu Asn Pro Tyr Leu Ala Ala Glu
            490                 495                 500
cgt ggc ctc atc gac gcg gtg atc ctg ccg tcc gag acc cgt ggc cag   1892
Arg Gly Leu Ile Asp Ala Val Ile Leu Pro Ser Glu Thr Arg Gly Gln
        505                 510                 515
atc gca cgc aac ctg cgt ctg ctc aag cac aag aat gtc tcc cgc cct   1940
Ile Ala Arg Asn Leu Arg Leu Leu Lys His Lys Asn Val Ser Arg Pro
    520                 525                 530
gcc cgc aag cac ggc aac atg cca ctg taagcacccg ggaccacccc         1987
Ala Arg Lys His Gly Asn Met Pro Leu
535                 540
ctacgcccgc acccacggcc ctttgctggc aggtgcgggc gctgtgcgtt ttccgcgcct 2047
gccgacgccc ggcccccctgc cctgtgatgc gatctgcgga tgtgatctgc gcccgcgcca 2107
actcccctgg ttgaaccctg c                                           2128
```

<210> 6
<211> 543
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 6

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Met Thr Ile Ser Ser Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile
  1               5                  10                  15
Asn Thr Thr Ala Gly Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu
             20                  25                  30
Ala His Phe Pro Met Gly Glu Lys Ala Val Glu Lys Val His Ala Ala
         35                  40                  45
Asn Arg Leu Thr Ala Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly
     50                  55                  60
Ser Phe Ile Glu Thr Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe
 65                  70                  75                  80
Gly Leu Gly Asn Lys Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp
                 85                  90                  95
Gly Thr Ile Asp Gly Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr
            100                 105                 110
Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys
        115                 120                 125
Ile Met Glu Leu Ala Ile Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr
    130                 135                 140
Glu Gly Ala Gly Ala Arg Ile Gln Asp Gly Ala Val Ser Leu Asp Phe
```

145 150 155 160
Ile Ser Gln Thr Phe Tyr Gln Asn Ile Gln Ala Ser Gly Val Ile Pro
165 170 175
Gln Ile Ser Val Ile Met Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly
180 185 190
Pro Ala Leu Thr Asp Phe Val Val Met Val Asp Lys Thr Ser Lys Met
195 200 205
Phe Val Thr Gly Pro Asp Val Ile Lys Thr Val Thr Gly Glu Glu Ile
210 215 220
Thr Gln Glu Glu Leu Gly Gly Ala Thr Thr His Met Val Thr Ala Gly
225 230 235 240
Asn Ser His Tyr Thr Val Ala Thr Asp Glu Glu Ala Leu Asp Trp Val
245 250 255
Gln Asp Leu Ile Ser Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro
260 265 270
Val Glu Glu Phe Asp Glu Glu Asp Gly Gly Ile Ala Glu Asn Ile Thr
275 280 285
Ala Asp Asp Leu Lys Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val
290 295 300
Pro Tyr Asp Val Arg Asp Val Ile Gln Cys Leu Thr Asp Asp Gly Glu
305 310 315 320
Tyr Leu Glu Ile Gln Ala Asp Arg Ala Glu Asn Val Val Ile Ala Phe
325 330 335
Gly Arg Ile Glu Gly Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr
340 345 350
Gln Phe Ala Gly Cys Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg
355 360 365
Phe Val Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val
370 375 380
Asp Val Pro Gly Phe Leu Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile
385 390 395 400
Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val
405 410 415
Pro Lys Ile Thr Val Thr Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys
420 425 430
Val Met Gly Ser Lys Gly Leu Gly Ala Asp Ile Asn Leu Ala Trp Pro
435 440 445
Thr Ala Gln Ile Ala Val Met Gly Ala Ala Gly Ala Val Gln Phe Ile
450 455 460
Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala Lys Gly Leu Asp Thr Val
465 470 475 480
Ala Leu Ala Gln Ser Phe Glu Arg Glu Tyr Glu Asp His Met Leu Asn
485 490 495

```
Pro Tyr Leu Ala Ala Glu Arg Gly Leu Ile Asp Ala Val Ile Leu Pro
            500                 505                 510
Ser Glu Thr Arg Gly Gln Ile Ala Arg Asn Leu Arg Leu Leu Lys His
        515                 520                 525
Lys Asn Val Ser Arg Pro Ala Arg Lys His Gly Asn Met Pro Leu
    530                 535                 540
```

<210> 7
<211> 2076
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (412)..(2022)

<400> 7

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acgcccggcc ccctgccctg tgatgcgatc tgcggatgtg atctgcgccc gcgccaactc 60
ccctggttga accctgccac ataccctgag tcgcacctgg gtggggtcac tttccacctc 120
acgggggga ggaggtcaca taggccatac gctgcacttt tgatgaagtg tgggcagatc 180
gaccgggcaa atctgggaaa taaggggcct ggtgaactag cattcccctt agcgaagggt 240
gagcatcgcg gaccccgcga tgtcccaacc ggtcgtaaat tcatgtgccg ccacagtccc 300
ctcaccaggg gatcggaacc agcccagcct gattccggcg tgacggacct caccgtgaac 360
aagtccccgc attactcaca gaactcacac caggatttag actaagaaac c atg act  417
                                                    Met Thr
                                                     1

gca gca acg aca gca cct gat ctg acc acc acc gcc ggc aaa ctc gcg   465
Ala Ala Thr Thr Ala Pro Asp Leu Thr Thr Thr Ala Gly Lys Leu Ala
          5                  10                  15

gat ctc cgc gcc cgc ctt tcc gag acc cag gcc ccc atg ggt cag gcc   513
Asp Leu Arg Ala Arg Leu Ser Glu Thr Gln Ala Pro Met Gly Gln Ala
     20                  25                  30

tcc gtg gag aag gtg cac gag gca ggg aag aag acc gca cgc gag cgc   561
Ser Val Glu Lys Val His Glu Ala Gly Lys Lys Thr Ala Arg Glu Arg
 35                  40                  45                  50

atc gag tac ctg ctc gat gag ggc tcc ttc gtt gag gtc gat gcc ctc   609
Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Val Asp Ala Leu
                 55                  60                  65

gcc cgc cac cgt tcc aag aac ttc ggc ctg gac tcc aag cgc ccg gtc   657
Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg Pro Val
             70                  75                  80

acc gac ggt gtg gtc acc ggt tac ggc acc atc gac gga cgc aag gtc   705
Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg Lys Val
```

```
          85                  90                  95
tgc gtc ttc tcc cag gac ggc gct atc ttc ggc ggt gcc ctc ggt gag   753
Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu Gly Glu
    100                 105                 110
gtc tac ggc gag aag atc gtc aag atc atg gac ctg gcc atc aag acc   801
Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile Lys Thr
115                 120                 125                 130
ggt gtc ccc ctc atc ggc atc aac gag ggc gcc ggc gcc cgc atc cag   849
Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg Ile Gln
                135                 140                 145
gaa ggc gtt gtc tcc ctg ggc ctg tac tcc cag atc ttc tac cgc aac   897
Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr Arg Asn
            150                 155                 160
acc cag gca tcc ggt gtc atc cca cag atc tcc ctc atc atg ggt gcc   945
Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Ala
        165                 170                 175
tgc gcc ggt ggc cat gtg tac tcc ccc gcc ctg acc gac ttc atc atc   993
Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe Ile Ile
    180                 185                 190
atg gtg gac aag acc tcc aag atg ttc atc acc ggc ccc gac gtg atc  1041
Met Val Asp Lys Thr Ser Lys Met Phe Ile Thr Gly Pro Asp Val Ile
195                 200                 205                 210
aag acc gtc acc ggc gag gag gtc acc cag gag gaa ctg ggt ggt gcc  1089
Lys Thr Val Thr Gly Glu Glu Val Thr Gln Glu Glu Leu Gly Gly Ala
                215                 220                 225
tac acc cac atg gcc cag tcc ggc acc tcg cac tac acc gca gcc gat  1137
Tyr Thr His Met Ala Gln Ser Gly Thr Ser His Tyr Thr Ala Ala Asp
            230                 235                 240
gac tcc gat gcc ctc gac tgg gtc cgt gag ctg gtc agc tac ctg ccg  1185
Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Val Ser Tyr Leu Pro
        245                 250                 255
tcc aac aac cgt gcg gag acc cca cgc cag gac gcc gac atc atg gtg  1233
Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Asp Ala Asp Ile Met Val
    260                 265                 270
ggc tcc atc aag gag aac atc acc gag acc gac ctc gaa ctc gac acc  1281
Gly Ser Ile Lys Glu Asn Ile Thr Glu Thr Asp Leu Glu Leu Asp Thr
275                 280                 285                 290
ctg atc ccg gat tcc ccg aac cag ccg tac gac atg aag gac gtc atc  1329
Leu Ile Pro Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Asp Val Ile
                295                 300                 305
acc cgc atc gtc gat gat gcc gag ttc ttc gag atc cag gag ggt tac  1377
Thr Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu Gly Tyr
            310                 315                 320
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gcc gag aac atc atc tgc ggt ttc gcc cgc gtc gag ggt cgt gcc gtg   1425
Ala Glu Asn Ile Ile Cys Gly Phe Ala Arg Val Glu Gly Arg Ala Val
        325                 330                 335
ggt atc gtg gcc aac cag ccg atg cag ttc gcc ggc tgc ctg gac atc   1473
Gly Ile Val Ala Asn Gln Pro Met Gln Phe Ala Gly Cys Leu Asp Ile
    340                 345                 350
aag gca tcc gag aag gcc gcc cgc ttc atc cgc acc tgt gac gcc ttc   1521
Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp Ala Phe
355                 360                 365                 370
aac atc ccg atc atc gag ctt gtc gac gtc cca ggc ttc ctc ccg ggc   1569
Asn Ile Pro Ile Ile Glu Leu Val Asp Val Pro Gly Phe Leu Pro Gly
                375                 380                 385
acc aac cag gag ttc gac ggc atc atc cgt cgc ggc gcg aag ctg ctc   1617
Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys Leu Leu
            390                 395                 400
tac gcc tac gcc gag gcc acc gtc ggc aag atc acc gtg atc acc cgc   1665
Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile Thr Arg
        405                 410                 415
aag tcc tac ggc ggt gcc tac tgc gtg atg ggc tcc aag gac atg ggt   1713
Lys Ser Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp Met Gly
    420                 425                 430
gcg gac ctc gtc ttc gca tgg ccc acc gcg cag atc gcc gtc atg ggt   1761
Ala Asp Leu Val Phe Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly
435                 440                 445                 450
gcc tcc ggt gcc gtc ggc ttc atc tac cgc aag gag ctc aag cag gct   1809
Ala Ser Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Lys Gln Ala
                455                 460                 465
gca gcg gcc ggc gag gat gtc acc gcg ctg atg aag aag tac gag cag   1857
Ala Ala Ala Gly Glu Asp Val Thr Ala Leu Met Lys Lys Tyr Glu Gln
            470                 475                 480
gag tac gag gag acc ctg gtc aac ccg tac atg gct gca gag cgt ggc   1905
Glu Tyr Glu Glu Thr Leu Val Asn Pro Tyr Met Ala Ala Glu Arg Gly
        485                 490                 495
tac gtc gac gcc gtc atc cca cca tcc gag acc cgt ggt cag atc atc   1953
Tyr Val Asp Ala Val Ile Pro Pro Ser Glu Thr Arg Gly Gln Ile Ile
    500                 505                 510
gag ggt ctg cgt ctg ctc gac cgc aag gtg gtc aac gtc ccg gcc aag   2001
Glu Gly Leu Arg Leu Leu Asp Arg Lys Val Val Asn Val Pro Ala Lys
515                 520                 525                 530
aag cac ggt aac atc ccg ctg taaaccgtct tcccctccgg caccacgccg      2052
Lys His Gly Asn Ile Pro Leu
                535
gagaaggctt tgtccgcagc tgtc                                       2076
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<210> 8
<211> 537
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 8

Met	Thr	Ala	Ala	Thr	Thr	Ala	Pro	Asp	Leu	Thr	Thr	Thr	Ala	Gly	Lys
1				5				10					15		
Leu	Ala	Asp	Leu	Arg	Ala	Arg	Leu	Ser	Glu	Thr	Gln	Ala	Pro	Met	Gly
			20					25					30		
Gln	Ala	Ser	Val	Glu	Lys	Val	His	Glu	Ala	Gly	Lys	Lys	Thr	Ala	Arg
		35					40					45			
Glu	Arg	Ile	Glu	Tyr	Leu	Leu	Asp	Glu	Gly	Ser	Phe	Val	Glu	Val	Asp
	50					55					60				
Ala	Leu	Ala	Arg	His	Arg	Ser	Lys	Asn	Phe	Gly	Leu	Asp	Ser	Lys	Arg
65					70					75					80
Pro	Val	Thr	Asp	Gly	Val	Val	Thr	Gly	Tyr	Gly	Thr	Ile	Asp	Gly	Arg
				85					90					95	
Lys	Val	Cys	Val	Phe	Ser	Gln	Asp	Gly	Ala	Ile	Phe	Gly	Gly	Ala	Leu
			100					105					110		
Gly	Glu	Val	Tyr	Gly	Glu	Lys	Ile	Val	Lys	Ile	Met	Asp	Leu	Ala	Ile
		115					120					125			
Lys	Thr	Gly	Val	Pro	Leu	Ile	Gly	Ile	Asn	Glu	Gly	Ala	Gly	Ala	Arg
	130					135					140				
Ile	Gln	Glu	Gly	Val	Val	Ser	Leu	Gly	Leu	Tyr	Ser	Gln	Ile	Phe	Tyr
145					150					155					160
Arg	Asn	Thr	Gln	Ala	Ser	Gly	Val	Ile	Pro	Gln	Ile	Ser	Leu	Ile	Met
				165					170					175	
Gly	Ala	Cys	Ala	Gly	Gly	His	Val	Tyr	Ser	Pro	Ala	Leu	Thr	Asp	Phe
			180					185					190		
Ile	Ile	Met	Val	Asp	Lys	Thr	Ser	Lys	Met	Phe	Ile	Thr	Gly	Pro	Asp
		195					200					205			
Val	Ile	Lys	Thr	Val	Thr	Gly	Glu	Glu	Val	Thr	Gln	Glu	Glu	Leu	Gly
	210					215					220				
Gly	Ala	Tyr	Thr	His	Met	Ala	Gln	Ser	Gly	Thr	Ser	His	Tyr	Thr	Ala
225					230					235					240
Ala	Asp	Asp	Ser	Asp	Ala	Leu	Asp	Trp	Val	Arg	Glu	Leu	Val	Ser	Tyr
				245					250					255	
Leu	Pro	Ser	Asn	Asn	Arg	Ala	Glu	Thr	Pro	Arg	Gln	Asp	Ala	Asp	Ile
			260					265					270		
Met	Val	Gly	Ser	Ile	Lys	Glu	Asn	Ile	Thr	Glu	Thr	Asp	Leu	Glu	Leu
		275					280					285			

Asp Thr Leu Ile Pro Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Asp
290 295 300
Val Ile Thr Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu
305 310 315 320
Gly Tyr Ala Glu Asn Ile Ile Cys Gly Phe Ala Arg Val Glu Gly Arg
325 330 335
Ala Val Gly Ile Val Ala Asn Gln Pro Met Gln Phe Ala Gly Cys Leu
340 345 350
Asp Ile Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp
355 360 365
Ala Phe Asn Ile Pro Ile Ile Glu Leu Val Asp Val Pro Gly Phe Leu
370 375 380
Pro Gly Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys
385 390 395 400
Leu Leu Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile
405 410 415
Thr Arg Lys Ser Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp
420 425 430
Met Gly Ala Asp Leu Val Phe Ala Trp Pro Thr Ala Gln Ile Ala Val
435 440 445
Met Gly Ala Ser Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Lys
450 455 460
Gln Ala Ala Ala Ala Ala Gly Glu Asp Val Thr Ala Leu Met Lys Lys Tyr
465 470 475 480
Glu Gln Glu Tyr Glu Glu Thr Leu Val Asn Pro Tyr Met Ala Ala Glu
485 490 495
Arg Gly Tyr Val Asp Ala Val Ile Pro Pro Ser Glu Thr Arg Gly Gln
500 505 510
Ile Ile Glu Gly Leu Arg Leu Leu Asp Arg Lys Val Val Asn Val Pro
515 520 525
Ala Lys Lys His Gly Asn Ile Pro Leu
530 535

<210> 9
<211> 1643
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (326)..(1363)

<400> 9

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tcagccaccc gccgatgaga cctgcagcga caacggtggc ggtgctgacc tggtcagcgt 120
ctttgagttt catatccatg tcagacagtc taaccactct ctccgacgcg tccgaacatg 180
ctgggggtggc ggacaccatg tccgttcggg cgttgccccg acgggggaaa atcgcaggca 240
gatgtgtccg atgtgggata aacccaccgg ttcgggcgtg tcttcgggat caatggcaca 300
gcattaaccg tgtgggggggt ttaat atg gga gcc atg cga att gcc act ctc   352
                          Met Gly Ala Met Arg Ile Ala Thr Leu
                            1               5
acg tca ggc ggc gac tgc ccc gga ctc aat gct gtc atc agg gga atc   400
Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val Ile Arg Gly Ile
 10                  15                  20                  25
gtc cgt acc gca agt aat gaa ttc ggt tcc acc gtc gtg ggt tat cag   448
Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val Val Gly Tyr Gln
                 30                  35                  40
gac ggc tgg gag ggc ctg ctg gcg gac cga cgt gtt cag ctc tat gac   496
Asp Gly Trp Glu Gly Leu Leu Ala Asp Arg Arg Val Gln Leu Tyr Asp
             45                  50                  55
gat gag gac atc gac cgc atc ctg ctc cgc ggt gga aca atc ctg ggc   544
Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly Thr Ile Leu Gly
         60                  65                  70
acc ggt cgt ctc cac ccc gac aag ttc aga gcc gga atc gac cag gtc   592
Thr Gly Arg Leu His Pro Asp Lys Phe Arg Ala Gly Ile Asp Gln Val
     75                  80                  85
aag gcg aat ctc gcc gat gcg gga att gac gca ctc atc ccg atc ggt   640
Lys Ala Asn Leu Ala Asp Ala Gly Ile Asp Ala Leu Ile Pro Ile Gly
 90                  95                  100                 105
ggc gag ggc acc ctc aag gga gcg aag tgg ctc gcc gac aac ggc atc   688
Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ala Asp Asn Gly Ile
                110                 115                 120
ccc gtg gtc ggt gtc ccg aaa acc atc gac aat gat gtc aac ggc acg   736
Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp Val Asn Gly Thr
            125                 130                 135
gat ttc acc ttc ggt ttc gat tcc gcg gtc tct gtg gcc acc gac gcc   784
Asp Phe Thr Phe Gly Phe Asp Ser Ala Val Ser Val Ala Thr Asp Ala
        140                 145                 150
atc gac cgg ctg cac acc acg gcg gaa tcc cac aac cgt gtg atg atc   832
Ile Asp Arg Leu His Thr Thr Ala Glu Ser His Asn Arg Val Met Ile
    155                 160                 165
gtc gag gtc atg ggc cgc cac gtc ggt tgg atc gca ctg cat gcc ggc   880
Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala Leu His Ala Gly
170                 175                 180                 185
atg gcc ggt gga gcc cac tac acc gtc atc ccc gag gtg ccc ttc gac   928
Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu Val Pro Phe Asp
```

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                    190                 195                 200
atc tcg gag atc tgc aag cgt atg gaa cgt cgc ttc cag atg ggg gag   976
Ile Ser Glu Ile Cys Lys Arg Met Glu Arg Arg Phe Gln Met Gly Glu
            205                 210                 215
aag tac ggc atc atc gtc gtc gcg gag ggt gcc ctg ccc aag gag gga  1024
Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu Pro Lys Glu Gly
        220                 225                 230
acc atg gag ctg cgt gag ggg gag gtg gat cag ttc ggt cac aag acc  1072
Thr Met Glu Leu Arg Glu Gly Glu Val Asp Gln Phe Gly His Lys Thr
    235                 240                 245
ttc acc ggc atc ggc cag cag atc gcc gac gag gtg cac agg cgt ctg  1120
Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Val His Arg Arg Leu
250                 255                 260                 265
ggt cat gat gtc cgc acc acg gtc ctg ggc cat atc cag cgt ggt ggc  1168
Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile Gln Arg Gly Gly
                270                 275                 280
acc ccc acc gcc ttc gac cgt gtc ctg gcc acc cgg tac ggt gtc cgc  1216
Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg Tyr Gly Val Arg
            285                 290                 295
gcc gcg cgt gcc tgc cac gag ggt cag ttc aac acc gtg gtc gcg ctc  1264
Ala Ala Arg Ala Cys His Glu Gly Gln Phe Asn Thr Val Val Ala Leu
        300                 305                 310
aag ggg gag cgc atc cgg atg atc tcc ttc gat gag gcc gtg ggc acc  1312
Lys Gly Glu Arg Ile Arg Met Ile Ser Phe Asp Glu Ala Val Gly Thr
    315                 320                 325
ctg aag aag gtg ccg atg gaa cgc tgg gtg acc gcc cag gct atg ttc  1360
Leu Lys Lys Val Pro Met Glu Arg Trp Val Thr Ala Gln Ala Met Phe
330                 335                 340                 345
ggt tagtcaggcc gcattcccgg ttccgcgccc gcgggggccgg gttttttcat      1413
Gly

gccccggaac acatcggtat gaaatcgtga tatgcattac ttgacgggga agtgggggat 1473
ccgtcacctc gcgttgtcca actacagccc gcagcgcctg cgggaattct tcgagcaatc 1533
cgccgattcc ccggccccgtc ccgtcgccgt ccaaccgcag tacaatctgc tggcccgccg 1593
ggattatgag accggtatcc gcccggtcgt ggacgagttc ggtcccgcgg            1643

<210> 10
<211> 346
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 10
Met Gly Ala Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro
 1               5                  10                  15
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Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu
20 25 30
Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu
35 40 45
Ala Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
50 55 60
Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
65 70 75 80
Lys Phe Arg Ala Gly Ile Asp Gln Val Lys Ala Asn Leu Ala Asp Ala
85 90 95
Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
100 105 110
Ala Lys Trp Leu Ala Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
115 120 125
Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
130 135 140
Ser Ala Val Ser Val Ala Thr Asp Ala Ile Asp Arg Leu His Thr Thr
145 150 155 160
Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
165 170 175
Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
180 185 190
Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ser Glu Ile Cys Lys Arg
195 200 205
Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val
210 215 220
Ala Glu Gly Ala Leu Pro Lys Glu Gly Thr Met Glu Leu Arg Glu Gly
225 230 235 240
Glu Val Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln
245 250 255
Ile Ala Asp Glu Val His Arg Arg Leu Gly His Asp Val Arg Thr Thr
260 265 270
Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg
275 280 285
Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu
290 295 300
Gly Gln Phe Asn Thr Val Val Ala Leu Lys Gly Glu Arg Ile Arg Met
305 310 315 320
Ile Ser Phe Asp Glu Ala Val Gly Thr Leu Lys Lys Val Pro Met Glu
325 330 335
Arg Trp Val Thr Ala Gln Ala Met Phe Gly
340 345

<210> 11
<211> 498
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (1)..(498)

<400> 11

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tac tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggt    48
Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
 1               5                  10                  15
tgg gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg    96
Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
            20                  25                  30
acg cac ctg ccc gat gct ctt tac ccg gat gta tcc tat gac ctg gat   144
Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser Tyr Asp Leu Asp
        35                  40                  45
gga tgc tat tcc ggc gga gcc gta ttt tct gac ggc acg ctt aaa ctt   192
Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly Thr Leu Lys Leu
    50                  55                  60
ttc tac acc ggc aac cga aaa att gac ggc aag cgc cgc gcc acc caa   240
Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
65                  70                  75                  80
aac ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat   288
Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
                85                  90                  95
cgc cgc tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttt   336
Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
            100                 105                 110
acg ccc cac tac cgc gat ccc atg atc agc cct gat ggg gat ggt tgg   384
Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
        115                 120                 125
aag atg gtt ctt ggg gct cag cgc gaa aac ctc acc ggt gca gcg gtt   432
Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
    130                 135                 140
cta tac cgc tcg gca gat ctt gaa aac tgg gaa ttc tcc ggt gaa atc   480
Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile
145                 150                 155                 160
acc ttt gac ctc agc gac                                          498
Thr Phe Asp Leu Ser Asp
                165
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<210> 12
<211> 166
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 12

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Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
 1               5                  10                  15
Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
            20                  25                  30
Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser Tyr Asp Leu Asp
        35                  40                  45
Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly Thr Leu Lys Leu
    50                  55                  60
Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
65                  70                  75                  80
Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
                85                  90                  95
Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
            100                 105                 110
Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
        115                 120                 125
Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
    130                 135                 140
Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile
145                 150                 155                 160
Thr Phe Asp Leu Ser Asp
                165
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<210> 13
<211> 479
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (1)..(477)

<400> 13

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Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
 1               5                  10                  15
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tgg gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg 96
Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
20 25 30

acg cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat 144
Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp
35 40 45

gga tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt 192
Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu
50 55 60

ttc tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa 240
Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
65 70 75 80

aac ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat 288
Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
85 90 95

cgc cgt tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttc 336
Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
100 105 110

aca ccc cat tac cgc gat ccc atg atc agc cct gat ggt gat ggt tgg 384
Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
115 120 125

aaa atg gtt ctt ggg gcc caa cgc gaa aac ctc acc ggt gca gcg gtt 432
Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
130 135 140

cta tac cgc tcg aca gat ctt gaa aac tgg gaa ttc tcc ggt gaa at 479
Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu
145 150 155

<210> 14
<211> 159
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 14
Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
1 5 10 15
Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
20 25 30
Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp
35 40 45
Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu
50 55 60
Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln

65 70 75 80
Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
85 90 95
Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
100 105 110
Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
115 120 125
Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
130 135 140
Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu
145 150 155

<210> 15
<211> 490
<212> DNA
<213> Corynebacterium thermoaminogenes
<400> 15
attttaatgg atattatcta tattttatca atattatcct tatgcacctg aatggggacc 60
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tttagaacct ggagatgaag aagaaaaatg gttgtttctc tggtacaggt atagtcaaag 180
atgataagtt gtatttattt tatacaggtc accattatta taatgacgat gatcccgatc 240
attttggca aaatcaaaat atggcttata gtgaagatgg cattcatttt caaaaatata 300
aacaaaatgc aatcattcct accccacctg aagataatac acatcacttc agagatccaa 360
aggtatggga acatccatgg cttattatta catgatagta ggtagtcaaa atgatagaga 420
attaggacgt attatcttat atcgttctga ggatttatag aggggaattc tggtcctgag 480
atcaatccaa 490

<210> 16
<211> 4254
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
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<222> (637)..(1362)

<220>
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<222> (1434)..(2315)

<220>
<221> CDS
<222> (2432)..(3115)

<220>
<221> CDS
<222> (3235)..(4065)
<400> 16

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tcacggcgcg cagattaccc agtgtgccgt agagacgctg atcggcattc tcacgcaccg 60
cgcaggtgtt gaagacgatg agatcagggg tgtcaccctc ccccgccgcg gtgtaaccgg 120
cctcctcgag cagaccggag agacgctcgg aatcgtggac gttcatctgg cagccgaagg 180
tacgcacctc ataggtgcgg gcagtggtgc cctcccggtt ccccccgcgcc gggaggggtgt 240
cggcgggggtg gtccgggtgg gatggatggg tgttcatctg gtgggtatca atctgctgcg 300
tcacgggagg taattgtatc ggccgcgggc accctgacat aaacgtccga tccagaggaa 360
cgcaaccccg tggagtgtcg cagccatgca ggttgggcaa caccgtaacg gaacctagca 420
gagtggtagg attgacttca cattctttac ctattgagct attgataaaa tccgggcgga 480
aatggaaatc acccccacaa atcaccccaa ctgacctgtg gaaagggcga gaaatccagg 540
gaaattcatt tcaaaatgga ctcaatcaca ggatttaccc cacatgaccc aacattcctt 600
tatgctatcc ccatgacgca gaccacaaat cacccg atg atc aag atg acg ggg   654
                                    Met Ile Lys Met Thr Gly
                                     1               5
gtg cag aag ttc ttc gat gac ttc cag gcc ctg acc gat atc aat ctt   702
Val Gln Lys Phe Phe Asp Asp Phe Gln Ala Leu Thr Asp Ile Asn Leu
            10                  15                  20
gag gtc ccc gcg gga cag gtc gtt gtt gtt ctc ggc ccg tcc ggt tcc   750
Glu Val Pro Ala Gly Gln Val Val Val Val Leu Gly Pro Ser Gly Ser
        25                  30                  35
gga aag tcg acg ctg tgc cgc acc atc aac cgc ctc gaa acc atc gag   798
Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn Arg Leu Glu Thr Ile Glu
    40                  45                  50
gag gga acc atc gag atc gat gga aaa ctg ctt ccg gag gag ggc aag   846
Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu Leu Pro Glu Glu Gly Lys
55                  60                  65                  70
gac ctg gcc aag atc cgt gcc gac gtg ggc atg gtg ttc cag tct ttc   894
Asp Leu Ala Lys Ile Arg Ala Asp Val Gly Met Val Phe Gln Ser Phe
                75                  80                  85
aac ctc ttc ccc cac ctc acc atc aag gac aat gtc acc ctc ggc ccg   942
Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn Val Thr Leu Gly Pro
            90                  95                  100
atg aag gtc cgg aag atg aag aag tcc gag gcc aat gag gtg gcc atg   990
Met Lys Val Arg Lys Met Lys Lys Ser Glu Ala Asn Glu Val Ala Met
        105                 110                 115
aag ctg ttg gaa cgc gtc ggc atc gcc aac cag gcc gag aaa tac ccg   1038
Lys Leu Leu Glu Arg Val Gly Ile Ala Asn Gln Ala Glu Lys Tyr Pro
    120                 125                 130
gca cag ctc tcg ggc ggg cag cag cag cgc gtg gcc atc gcc cgc gca   1086
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Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala
135                 140                 145                 150
ctg gcg atg aac ccc aag atc atg ctt ttc gac gaa cca acc tcc gcc   1134
Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp Glu Pro Thr Ser Ala
                155                 160                 165
ctc gac ccc gag atg gtc aac gag gtt ctg gac gtc atg gcg agt ctg   1182
Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp Val Met Ala Ser Leu
            170                 175                 180
gcc aag gaa ggc atg acc atg gtg tgt gtc acc cac gag atg ggt ttc   1230
Ala Lys Glu Gly Met Thr Met Val Cys Val Thr His Glu Met Gly Phe
        185                 190                 195
gca cgc agg gcc gca gac cgt gtg ctg ttc atg tct gac ggc gcc atc   1278
Ala Arg Arg Ala Ala Asp Arg Val Leu Phe Met Ser Asp Gly Ala Ile
    200                 205                 210
gtc gag gac tcc gac ccg gag acc ttc ttc acc aat cca caa acc gac   1326
Val Glu Asp Ser Asp Pro Glu Thr Phe Phe Thr Asn Pro Gln Thr Asp
215                 220                 225                 230
cgg gcg aag gat ttc ctg ggc aag atc ctc gcc cac tgacctcccc        1372
Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala His
                235                 240
tcactctgtg tccaactccc ccgctggcca aaatcagcga ccatgaccaa caggagcatc 1432
a atg tcg cac aaa cgc atg ttc acc cgt ctc gcc gca gcc acc agc gca   1481
  Met Ser His Lys Arg Met Phe Thr Arg Leu Ala Ala Ala Thr Ser Ala
        245                 250                 255
gct gtt ctc gcc ggc atc acc ctc acc gcc tgt ggt gat tcc gag ggt   1529
Ala Val Leu Ala Gly Ile Thr Leu Thr Ala Cys Gly Asp Ser Glu Gly
    260                 265                 270
ggt gac ggt ctg ctc gcc gcc atc gaa aat ggc aat gtc acc atc ggc   1577
Gly Asp Gly Leu Leu Ala Ala Ile Glu Asn Gly Asn Val Thr Ile Gly
275                 280                 285                 290
acc aag tac gat cag ccg ggt ctg gga ctg cgt aac ccg gac aat tcc   1625
Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser
                295                 300                 305
atg agc gga ctg gat gtc gac gtc gcg cag tac gtg gtc aac tcc atc   1673
Met Ser Gly Leu Asp Val Asp Val Ala Gln Tyr Val Val Asn Ser Ile
            310                 315                 320
gcc gat gac aac ggt tgg gat cac ccc acc gtg gaa tgg cgc gag acc   1721
Ala Asp Asp Asn Gly Trp Asp His Pro Thr Val Glu Trp Arg Glu Thr
        325                 330                 335
ccc tcc gcc cag cgc gag acc ctc atc cag aac ggt gag gtg gat atg   1769
Pro Ser Ala Gln Arg Glu Thr Leu Ile Gln Asn Gly Glu Val Asp Met
    340                 345                 350
atc gcc gca acc tac tcc atc aac ccc gga cgc tcc gaa tcg gtg aac   1817
```

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Ile Ala Ala Thr Tyr Ser Ile Asn Pro Gly Arg Ser Glu Ser Val Asn
355                 360                 365                 370
ttc ggt gga cca tac ctc ctc acc cac cag gcc ctc ctg gtc cgc gag   1865
Phe Gly Gly Pro Tyr Leu Leu Thr His Gln Ala Leu Leu Val Arg Glu
                375                 380                 385
gac gat gac cgc atc cag acc ctc gag gac ctc gat gac ggc ctg atc   1913
Asp Asp Asp Arg Ile Gln Thr Leu Glu Asp Leu Asp Asp Gly Leu Ile
            390                 395                 400
ctg tgt tcc gtt acc gga tcc acc ccc gcc cag aag gtc aag gat gtc   1961
Leu Cys Ser Val Thr Gly Ser Thr Pro Ala Gln Lys Val Lys Asp Val
        405                 410                 415
ctc ccc ggc gtc cag ctg cag gaa tac gac acc tac tcc tcc tgt gtg   2009
Leu Pro Gly Val Gln Leu Gln Glu Tyr Asp Thr Tyr Ser Ser Cys Val
    420                 425                 430
gag gca ctg agc cag ggc aac gtc gat gca atg acc acc gac gcc acc   2057
Glu Ala Leu Ser Gln Gly Asn Val Asp Ala Met Thr Thr Asp Ala Thr
435                 440                 445                 450
atc ctc ttc ggc tac gcg cag cag cgc gaa ggt gaa ttc cgc gtc gtg   2105
Ile Leu Phe Gly Tyr Ala Gln Gln Arg Glu Gly Glu Phe Arg Val Val
                455                 460                 465
gag atg gaa cag gac ggc gag ccg ttc acc aat gag tac tac ggc atc   2153
Glu Met Glu Gln Asp Gly Glu Pro Phe Thr Asn Glu Tyr Tyr Gly Ile
            470                 475                 480
ggt atc acc aag gat gac acc gaa gcc acc gat gcg atc aac gca gcg   2201
Gly Ile Thr Lys Asp Asp Thr Glu Ala Thr Asp Ala Ile Asn Ala Ala
        485                 490                 495
ttg gag cgt atg tac gcc gac ggt tcc ttc cag cgt ttc ctc acc gag   2249
Leu Glu Arg Met Tyr Ala Asp Gly Ser Phe Gln Arg Phe Leu Thr Glu
    500                 505                 510
aac ctc ggc gag gat tcc cag gtt gtc cag gag ggc acc ccg ggt gac   2297
Asn Leu Gly Glu Asp Ser Gln Val Val Gln Glu Gly Thr Pro Gly Asp
515                 520                 525                 530
ctc tcc ttc ctg gac gag tgacctgacg gggccgaacg cccgatgagc          2345
Leu Ser Phe Leu Asp Glu
                535
atgcgtggcc cccgcatccc ggggtgccac gcatcatcac tttcaccact gatcccctac 2405
cgttccttac cgaggagaaa ttcccc atg agt aca tta tgg gcg gat ctg ggt   2458
                          Met Ser Thr Leu Trp Ala Asp Leu Gly
                                540                 545
ccg tca ctc cta ccc gca ttc tgg gtg aca atc caa ctc acc gtc tat   2506
Pro Ser Leu Leu Pro Ala Phe Trp Val Thr Ile Gln Leu Thr Val Tyr
                550                 555                 560
tcc gcc atc gga tcc atg atc ctc ggt acc atc ctc acc gcc atg agg   2554
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Ser Ala Ile Gly Ser Met Ile Leu Gly Thr Ile Leu Thr Ala Met Arg
                565                 570                 575
gtg tcc ccg gtg aag atc ctg cgc agc ata tcc acc gcc tac atc aac   2602
Val Ser Pro Val Lys Ile Leu Arg Ser Ile Ser Thr Ala Tyr Ile Asn
        580                 585                 590
acg gtc cgt aac acc cca ctg acc ctg gtg atc ctg ttc tgt tcc ttc   2650
Thr Val Arg Asn Thr Pro Leu Thr Leu Val Ile Leu Phe Cys Ser Phe
    595                 600                 605
ggc ctg tat cag aat ctc ggt ctc acc ctc gcc ggt cgc gac agt tcc   2698
Gly Leu Tyr Gln Asn Leu Gly Leu Thr Leu Ala Gly Arg Asp Ser Ser
610                 615                 620                 625
acc ttt ctg gcc gat aac aac ttc cgg ctc gcg gtg ctc gga ttc atc   2746
Thr Phe Leu Ala Asp Asn Asn Phe Arg Leu Ala Val Leu Gly Phe Ile
                630                 635                 640
ctg tac acc tcc gcc ttc gtt gcg gaa tca ctc cgg tca ggc atc aac   2794
Leu Tyr Thr Ser Ala Phe Val Ala Glu Ser Leu Arg Ser Gly Ile Asn
            645                 650                 655
acc gtg cac ttc ggg cag gcg gag gcc gcc cgg tcg ctg gga ctc ggt   2842
Thr Val His Phe Gly Gln Ala Glu Ala Ala Arg Ser Leu Gly Leu Gly
        660                 665                 670
ttc agt gac atc ttc cgg tcc atc atc ttc ccc cag gcg gtg cgt gcc   2890
Phe Ser Asp Ile Phe Arg Ser Ile Ile Phe Pro Gln Ala Val Arg Ala
    675                 680                 685
gcc atc atc ccg ctg ggc aac acc ctc atc gcc ctg acc aag aac acc   2938
Ala Ile Ile Pro Leu Gly Asn Thr Leu Ile Ala Leu Thr Lys Asn Thr
690                 695                 700                 705
acg atc gcg tcc gtg atc ggc gtc ggt gag gcc tcg ctg ctg atg aag   2986
Thr Ile Ala Ser Val Ile Gly Val Gly Glu Ala Ser Leu Leu Met Lys
                710                 715                 720
tcc acg att gaa aat cat gcc aac atg ctc ttc gtc gtg ttc gcc atc   3034
Ser Thr Ile Glu Asn His Ala Asn Met Leu Phe Val Val Phe Ala Ile
            725                 730                 735
ttc gcc gtc ggc ttc atg atc ctc acc ctc ccc atg ggc ctg ggg ctt   3082
Phe Ala Val Gly Phe Met Ile Leu Thr Leu Pro Met Gly Leu Gly Leu
        740                 745                 750
gga aaa ctc gct gag aaa atg gcg gtg aag aaa taatgtcctc ctccgtacgc 3135
Gly Lys Leu Ala Glu Lys Met Ala Val Lys Lys
    755                 760
gcaacagtcc tctacgacgc ccccggcccc cggggacgca ggtccaacac catcatcacc 3195
atcgccacca ccctggtggc agtggccgtc ctgttctgg gtg ggc agt gtt ctc     3249
                                          Val Gly Ser Val Leu
                                          765
cag gaa aac ggc cag ttg gac ggc gac aaa tgg acc ccg ttc ctc gat    3297
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Gln Glu Asn Gly Gln Leu Asp Gly Asp Lys Trp Thr Pro Phe Leu Asp
770                 775                 780                 785
ccc cag acc tgg acc acc tat ctt ctg ccc ggc ctg tgg gga acc ctg   3345
Pro Gln Thr Trp Thr Thr Tyr Leu Leu Pro Gly Leu Trp Gly Thr Leu
                790                 795                 800
aag gca gcg gtg gcc tcc atc ctt ctc gcg ctg atc atg ggc acc ctg   3393
Lys Ala Ala Val Ala Ser Ile Leu Leu Ala Leu Ile Met Gly Thr Leu
            805                 810                 815
ctc ggg ctc gga cgc atc tcc gaa atc cgg ctc ctg cgc tgg ttc tgc   3441
Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu Leu Arg Trp Phe Cys
        820                 825                 830
ggg atc atc atc gag acc ttc cgt gcc atc ccg gtg ctg atc ctc atg   3489
Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro Val Leu Ile Leu Met
    835                 840                 845
atc ttc gcc tat cag ttg ttc gcc cgt tac cag ctc gtt cca tca cgc   3537
Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln Leu Val Pro Ser Arg
850                 855                 860                 865
cag ctg gcc ttc gcc gcg gtg gtc ttc ggt ctc acc atg tac aac ggc   3585
Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu Thr Met Tyr Asn Gly
                870                 875                 880
tcc gtc atc gcc gag atc ctt aga tcg ggt atc gcc tcc ctg ccg aag   3633
Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile Ala Ser Leu Pro Lys
            885                 890                 895
gga cag cgt gag gcg gcg atc gcc ctg ggc atg tca acc cgc cag acc   3681
Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met Ser Thr Arg Gln Thr
        900                 905                 910
acc tgg tcg atc ctg ctc ccc cag gcg gtg gca gcg atg ctg ccc gcc   3729
Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala Ala Met Leu Pro Ala
    915                 920                 925
ctg atc gcg cag atg gtc atc gcg ctg aag gac tcc gcc ctc ggt tac   3777
Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp Ser Ala Leu Gly Tyr
930                 935                 940                 945
cag atc ggt tat atc gag gtg gta cgc tcc ggt atc cag tcc gca tcc   3825
Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly Ile Gln Ser Ala Ser
                950                 955                 960
gtc aac cgg aac tac ctg gct gcc ctc gcg gtg gtc gcg gtc atc atg   3873
Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val Val Ala Val Ile Met
            965                 970                 975
atc ctg atc aac ttc gca ctg acc gca ctg gca gag cgt atc cag cgt   3921
Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala Glu Arg Ile Gln Arg
        980                 985                 990
cag ctg cgt gcc gga cgt gcc cgc agg aac att gtg gca aag gtg ccc   3969
Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile Val Ala Lys Val Pro
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995 1000 1005

gag gaa ccc gat cag ggc ctg gat acc aag gac aat gtg aac gtg gat 4017
Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp Asn Val Asn Val Asp
1010 1015 1020 1025
tgg cac gat ccc gat tac aag gaa gtc aaa cac ccg gga ccg tca ttc 4065
Trp His Asp Pro Asp Tyr Lys Glu Val Lys His Pro Gly Pro Ser Phe
1030 1035 1040
tgacaggtcc ctggatcccc gctgcggtca ggaggcgggt gcaacaatga agtccggctg 4125
cccagatgtc tggggcagcc ggactttgtg gcagatcaat gctgactgag gtcctcgatg 4185
cgctcatcga gagcctcccg ggccaggtcc atcgacatac ccgcggggaa tccacgacgg 4245
gcaagtgct 4254

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<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 17
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20 25 30
Leu Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn
35 40 45
Arg Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu
50 55 60
Leu Pro Glu Glu Gly Lys Asp Leu Ala Lys Ile Arg Ala Asp Val Gly
65 70 75 80
Met Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp
85 90 95
Asn Val Thr Leu Gly Pro Met Lys Val Arg Lys Met Lys Lys Ser Glu
100 105 110
Ala Asn Glu Val Ala Met Lys Leu Leu Glu Arg Val Gly Ile Ala Asn
115 120 125
Gln Ala Glu Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg
130 135 140
Val Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe
145 150 155 160
Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu
165 170 175
Asp Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val
180 185 190
Thr His Glu Met Gly Phe Ala Arg Arg Ala Ala Asp Arg Val Leu Phe

195 200 205

Met Ser Asp Gly Ala Ile Val Glu Asp Ser Asp Pro Glu Thr Phe Phe
210 215 220
Thr Asn Pro Gln Thr Asp Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu
225 230 235 240
Ala His

<210> 18
<211> 294
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 18
Met Ser His Lys Arg Met Phe Thr Arg Leu Ala Ala Ala Thr Ser Ala
1 5 10 15
Ala Val Leu Ala Gly Ile Thr Leu Thr Ala Cys Gly Asp Ser Glu Gly
20 25 30
Gly Asp Gly Leu Leu Ala Ala Ile Glu Asn Gly Asn Val Thr Ile Gly
35 40 45
Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser
50 55 60
Met Ser Gly Leu Asp Val Asp Val Ala Gln Tyr Val Val Asn Ser Ile
65 70 75 80
Ala Asp Asp Asn Gly Trp Asp His Pro Thr Val Glu Trp Arg Glu Thr
85 90 95
Pro Ser Ala Gln Arg Glu Thr Leu Ile Gln Asn Gly Glu Val Asp Met
100 105 110
Ile Ala Ala Thr Tyr Ser Ile Asn Pro Gly Arg Ser Glu Ser Val Asn
115 120 125
Phe Gly Gly Pro Tyr Leu Leu Thr His Gln Ala Leu Leu Val Arg Glu
130 135 140
Asp Asp Asp Arg Ile Gln Thr Leu Glu Asp Leu Asp Asp Gly Leu Ile
145 150 155 160
Leu Cys Ser Val Thr Gly Ser Thr Pro Ala Gln Lys Val Lys Asp Val
165 170 175
Leu Pro Gly Val Gln Leu Gln Glu Tyr Asp Thr Tyr Ser Ser Cys Val
180 185 190
Glu Ala Leu Ser Gln Gly Asn Val Asp Ala Met Thr Thr Asp Ala Thr
195 200 205
Ile Leu Phe Gly Tyr Ala Gln Gln Arg Glu Gly Glu Phe Arg Val Val
210 215 220
Glu Met Glu Gln Asp Gly Glu Pro Phe Thr Asn Glu Tyr Tyr Gly Ile
225 230 235 240

Gly Ile Thr Lys Asp Asp Thr Glu Ala Thr Asp Ala Ile Asn Ala Ala
245 250 255
Leu Glu Arg Met Tyr Ala Asp Gly Ser Phe Gln Arg Phe Leu Thr Glu
260 265 270
Asn Leu Gly Glu Asp Ser Gln Val Val Gln Glu Gly Thr Pro Gly Asp
275 280 285
Leu Ser Phe Leu Asp Glu
290

<210> 19
<211> 228
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 19
Met Ser Thr Leu Trp Ala Asp Leu Gly Pro Ser Leu Leu Pro Ala Phe
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Trp Val Thr Ile Gln Leu Thr Val Tyr Ser Ala Ile Gly Ser Met Ile
20 25 30
Leu Gly Thr Ile Leu Thr Ala Met Arg Val Ser Pro Val Lys Ile Leu
35 40 45
Arg Ser Ile Ser Thr Ala Tyr Ile Asn Thr Val Arg Asn Thr Pro Leu
50 55 60
Thr Leu Val Ile Leu Phe Cys Ser Phe Gly Leu Tyr Gln Asn Leu Gly
65 70 75 80
Leu Thr Leu Ala Gly Arg Asp Ser Ser Thr Phe Leu Ala Asp Asn Asn
85 90 95
Phe Arg Leu Ala Val Leu Gly Phe Ile Leu Tyr Thr Ser Ala Phe Val
100 105 110
Ala Glu Ser Leu Arg Ser Gly Ile Asn Thr Val His Phe Gly Gln Ala
115 120 125
Glu Ala Ala Arg Ser Leu Gly Leu Gly Phe Ser Asp Ile Phe Arg Ser
130 135 140
Ile Ile Phe Pro Gln Ala Val Arg Ala Ala Ile Ile Pro Leu Gly Asn
145 150 155 160
Thr Leu Ile Ala Leu Thr Lys Asn Thr Thr Ile Ala Ser Val Ile Gly
165 170 175
Val Gly Glu Ala Ser Leu Leu Met Lys Ser Thr Ile Glu Asn His Ala
180 185 190
Asn Met Leu Phe Val Val Phe Ala Ile Phe Ala Val Gly Phe Met Ile
195 200 205
Leu Thr Leu Pro Met Gly Leu Gly Leu Gly Lys Leu Ala Glu Lys Met
210 215 220

Ala Val Lys Lys
225

<210> 20
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<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 20

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Thr	Pro	Phe	Leu	Asp	Pro	Gln	Thr	Trp	Thr	Thr	Tyr	Leu	Leu	Pro	Gly
		20					25					30			
Leu	Trp	Gly	Thr	Leu	Lys	Ala	Ala	Val	Ala	Ser	Ile	Leu	Leu	Ala	Leu
	35					40					45				
Ile	Met	Gly	Thr	Leu	Leu	Gly	Leu	Gly	Arg	Ile	Ser	Glu	Ile	Arg	Leu
50					55					60					
Leu	Arg	Trp	Phe	Cys	Gly	Ile	Ile	Ile	Glu	Thr	Phe	Arg	Ala	Ile	Pro
65				70					75						80
Val	Leu	Ile	Leu	Met	Ile	Phe	Ala	Tyr	Gln	Leu	Phe	Ala	Arg	Tyr	Gln
				85				90					95		
Leu	Val	Pro	Ser	Arg	Gln	Leu	Ala	Phe	Ala	Ala	Val	Val	Phe	Gly	Leu
			100					105					110		
Thr	Met	Tyr	Asn	Gly	Ser	Val	Ile	Ala	Glu	Ile	Leu	Arg	Ser	Gly	Ile
		115					120					125			
Ala	Ser	Leu	Pro	Lys	Gly	Gln	Arg	Glu	Ala	Ala	Ile	Ala	Leu	Gly	Met
	130					135					140				
Ser	Thr	Arg	Gln	Thr	Thr	Trp	Ser	Ile	Leu	Leu	Pro	Gln	Ala	Val	Ala
145					150					155					160
Ala	Met	Leu	Pro	Ala	Leu	Ile	Ala	Gln	Met	Val	Ile	Ala	Leu	Lys	Asp
				165					170					175	
Ser	Ala	Leu	Gly	Tyr	Gln	Ile	Gly	Tyr	Ile	Glu	Val	Val	Arg	Ser	Gly
			180					185					190		
Ile	Gln	Ser	Ala	Ser	Val	Asn	Arg	Asn	Tyr	Leu	Ala	Ala	Leu	Ala	Val
		195					200					205			
Val	Ala	Val	Ile	Met	Ile	Leu	Ile	Asn	Phe	Ala	Leu	Thr	Ala	Leu	Ala
	210					215					220				
Glu	Arg	Ile	Gln	Arg	Gln	Leu	Arg	Ala	Gly	Arg	Ala	Arg	Arg	Asn	Ile
225					230					235					240
Val	Ala	Lys	Val	Pro	Glu	Glu	Pro	Asp	Gln	Gly	Leu	Asp	Thr	Lys	Asp
				245					250					255	
Asn	Val	Asn	Val	Asp	Trp	His	Asp	Pro	Asp	Tyr	Lys	Glu	Val	Lys	His
			260					265					270		

Pro Gly Pro Ser Phe
275

<210> 21
<211> 3598
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<213> Corynebacterium thermoaminogenes
<220>
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<222> (454)..(3222)
<400> 21

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tccataatgt ggcctgtaac accettgggc tcaaggcttc cacgccccac cgggaccctc 180
atcagcaggt gaaacagacc ctcctgcaat gctttgttaa aaagaaccgc cctttgtgcg 240
tatccttgtg tcaattgtgc gcgcactgcc accagcttic ctcaggattg aacacggtcg 300
ggaaatcctc cccggatacc ctgcacgccc cacctcccac accgacaccg gcggggaggg 360
ccgggcacgt tttcagctgc gggtgatgga agcggtcgcc ggtcccccgg tcgcataaac 420
gaaatgaaaa acattccaac aggaggtgtg gaa atg gcc gat caa gca aaa ctt  474
                                  Met Ala Asp Gln Ala Lys Leu
                                   1               5
ggt ggc aaa ccc aca gat gac acc aac ttc gcg atg atc cgt gat ggc   522
Gly Gly Lys Pro Thr Asp Asp Thr Asn Phe Ala Met Ile Arg Asp Gly
            10                  15                  20
gtt gca tct tat ttg aac gac tcc gac ccg gag gag acc aag gag tgg   570
Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Lys Glu Trp
        25                  30                  35
atg gac tcc cta gac ggt cta ctg cag gat tcc tct ccg gag cgc gcc   618
Met Asp Ser Leu Asp Gly Leu Leu Gln Asp Ser Ser Pro Glu Arg Ala
    40                  45                  50                  55
cgt tac ctg atg ctg cgc ctg ctg gag cgg gca tcc gcc aag cgt gtc   666
Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys Arg Val
                60                  65                  70
cca ctg ccc ccg atg acg tcc acc gat tac gtc aac acc atc ccc aca   714
Pro Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile Pro Thr
            75                  80                  85
tcc atg gag ccc gat ttc ccg ggt gat gag gag atg gag aag cgc tac   762
Ser Met Glu Pro Asp Phe Pro Gly Asp Glu Glu Met Glu Lys Arg Tyr
        90                  95                  100
cgc cgc tgg atg cgc tgg aac gcc gcc atc atg gtg cac cgt gcc cag   810
Arg Arg Trp Met Arg Trp Asn Ala Ala Ile Met Val His Arg Ala Gln
    105                 110                 115
cgc ccg gga atc ggt gtg ggt ggg cac atc tcc acc tac gcc ggc gcc   858
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Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala Gly Ala
120                 125                 130                 135
gcc cca ctc tac gag gtc ggt ttc aac cac ttc ttc cgc ggc aag gac    906
Ala Pro Leu Tyr Glu Val Gly Phe Asn His Phe Phe Arg Gly Lys Asp
                140                 145                 150
cac ccg ggt ggc ggt gac cag gtc ttc ttc cag ggt cac gcc tcc ccg    954
His Pro Gly Gly Gly Asp Gln Val Phe Phe Gln Gly His Ala Ser Pro
            155                 160                 165
ggc atg tac gcc cgc gcc ttc ctc gag ggc cgt ctc acc gag agc gat   1002
Gly Met Tyr Ala Arg Ala Phe Leu Glu Gly Arg Leu Thr Glu Ser Asp
        170                 175                 180
ctg gac agc ttc cgc cag gag gtc tcc tac gaa ggt ggt ggc atc ccg   1050
Leu Asp Ser Phe Arg Gln Glu Val Ser Tyr Glu Gly Gly Gly Ile Pro
    185                 190                 195
tcc tac ccg cac ccg cac ggc atg ccg gac ttc tgg gag ttc ccg acc   1098
Ser Tyr Pro His Pro His Gly Met Pro Asp Phe Trp Glu Phe Pro Thr
200                 205                 210                 215
gtg tcc atg ggc ctc ggg ccc atg gat gcc atc tac cag gcg cgc ttc   1146
Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg Phe
                220                 225                 230
aac cgc tac ctg cac aac cgt ggc atc aag gac acc tcg gag cag cac   1194
Asn Arg Tyr Leu His Asn Arg Gly Ile Lys Asp Thr Ser Glu Gln His
            235                 240                 245
gtc tgg gca ttc ctc ggt gac ggc gag atg gat gag ccg gag tcc cgt   1242
Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser Arg
        250                 255                 260
ggt ctc atc cac cag gct gcg ctg aac aac ctg gac aac ctc acc ttc   1290
Gly Leu Ile His Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr Phe
    265                 270                 275
gtg atc aac tgc aac ctg cag cgt ctt gat ggc ccg gtc cgc ggt aac   1338
Val Ile Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly Asn
280                 285                 290                 295
acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggt gcc ggc tgg   1386
Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly Trp
                300                 305                 310
tcc gtc atc aag gtc atc tgg ggc cgt gag tgg gat gaa ctg ctg gag   1434
Ser Val Ile Lys Val Ile Trp Gly Arg Glu Trp Asp Glu Leu Leu Glu
            315                 320                 325
aag gac cag gac ggt gct ctt gtc gag gtc atg aac aac acc tcc gac   1482
Lys Asp Gln Asp Gly Ala Leu Val Glu Val Met Asn Asn Thr Ser Asp
        330                 335                 340
ggt gac tac cag acc ttc aag gcc aat gac ggt gcc tac gtc cgt gag   1530
Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg Glu
```

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    345                 350                 355
cac ttc ttc ggc cgt gac ccc cgc acc ctc aag ctc gtc gag gac atg   1578
His Phe Phe Gly Arg Asp Pro Arg Thr Leu Lys Leu Val Glu Asp Met
360                 365                 370                 375
acc gac gag gag atc tgg aag ctg ccc cgt ggt ggc cat gac tac cgt   1626
Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr Arg
                380                 385                 390
aag gtc tac gcc gcc tac aag cgt gcg ctg gag acc aag gac cgc ccg   1674
Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg Pro
            395                 400                 405
acc gtc att ctc gcc cat acc atc aag ggc tac ggc ctg ggc cac aac   1722
Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His Asn
        410                 415                 420
ttc gag ggc cgc aac gcg acc cac cag atg aag aag ctg acc ctg gat   1770
Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu Asp
    425                 430                 435
gac ctg aag ctg ttc cgt gac aag cag ggt ctg ccc atc acc gat gag   1818
Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Leu Pro Ile Thr Asp Glu
440                 445                 450                 455
gag ctg gag aag gat ccc tac ctg cct ccg tac tac cac ccg ggt gag   1866
Glu Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly Glu
                460                 465                 470
gac gca ccg gag atc aag tac atg aag gag cgt cgc cag gcg ctc ggt   1914
Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Gln Ala Leu Gly
            475                 480                 485
ggt ttc ctg ccg gag cgc cgt gag aag tac gag cca ctg cag gtt ccc   1962
Gly Phe Leu Pro Glu Arg Arg Glu Lys Tyr Glu Pro Leu Gln Val Pro
        490                 495                 500
ccg ctg gac aag ctg cgg tcc gtg cgc aag ggt tcc ggc aag cag cag   2010
Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln Gln
    505                 510                 515
gtg gcc acc acc atg gcc acg gtg cgt acc ttc aag gaa ctc atg cgg   2058
Val Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met Arg
520                 525                 530                 535
gac aag aac ctg gcc gac cgc ttg gtc ccg atc atc ccg gat gag gcc   2106
Asp Lys Asn Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu Ala
                540                 545                 550
cgc acc ttc ggc ctg gac tcc tgg ttc ccg acc ctg aaa atc tac aac   2154
Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr Asn
            555                 560                 565
ccg cac ggt cag aac tac gtg ccg gtc gac cat gac ctc atg ctg tcc   2202
Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu Ser
        570                 575                 580
```

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tac cgt gag gcc aag gac ggc cag atc ctg cat gag ggc atc aac gag   2250
Tyr Arg Glu Ala Lys Asp Gly Gln Ile Leu His Glu Gly Ile Asn Glu
    585                 590                 595
gcc ggt tcc gtg gca tcg ttt atc gcc gcc gga acc tcc tac gcc acc   2298
Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala Thr
600                 605                 610                 615
cat ggc gag gcc atg atc ccg ctg tac atc ttc tac tcg atg ttc ggc   2346
His Gly Glu Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe Gly
                620                 625                 630
ttc cag cgc acc ggt gac ggc atc tgg gcc gca gcc gac cag atg acg   2394
Phe Gln Arg Thr Gly Asp Gly Ile Trp Ala Ala Ala Asp Gln Met Thr
            635                 640                 645
cgt ggt ttc ctc ctg ggc gcc acc gcc ggt cgc acc acc ctg acc ggt   2442
Arg Gly Phe Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly
        650                 655                 660
gag ggc ctc cag cac atg gat ggc cac tcc ccg atc ctg gcc tcc acc   2490
Glu Gly Leu Gln His Met Asp Gly His Ser Pro Ile Leu Ala Ser Thr
    665                 670                 675
aac ccc ggt gtg gag acc tat gac ccg gcg ttc tcc tac gag atc gcg   2538
Asn Pro Gly Val Glu Thr Tyr Asp Pro Ala Phe Ser Tyr Glu Ile Ala
680                 685                 690                 695
cac ctg gtc cac cgc ggc atc gac cgc atg tac gga ccg ggc aag ggt   2586
His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly
                700                 705                 710
gag aat gtc atc tac tac ctc acc atc tac aac gag cca acc ccg cag   2634
Glu Asn Val Ile Tyr Tyr Leu Thr Ile Tyr Asn Glu Pro Thr Pro Gln
            715                 720                 725
ccg gct gag cct gag gat ctg gac gtc gag ggc ctg cac aag ggc atc   2682
Pro Ala Glu Pro Glu Asp Leu Asp Val Glu Gly Leu His Lys Gly Ile
        730                 735                 740
tac ctc tac gac aag gcc gcc gag ggt gag ggc cat gag gcc tcg atc   2730
Tyr Leu Tyr Asp Lys Ala Ala Glu Gly Glu Gly His Glu Ala Ser Ile
    745                 750                 755
ctg gcc tcc ggc atc ggc atg cag tgg gca ctg cgc gcc cgt gac atc   2778
Leu Ala Ser Gly Ile Gly Met Gln Trp Ala Leu Arg Ala Arg Asp Ile
760                 765                 770                 775
ctc gcc gag gat tac ggc atc cgt gcc aac atc ttc tcc gcc acc tcg   2826
Leu Ala Glu Asp Tyr Gly Ile Arg Ala Asn Ile Phe Ser Ala Thr Ser
                780                 785                 790
tgg gtg gag ctg gcc cgc gac ggt gcc cgc cgt aac ctg gag gcg ctg   2874
Trp Val Glu Leu Ala Arg Asp Gly Ala Arg Arg Asn Leu Glu Ala Leu
            795                 800                 805
cgc aac ccg ggt gcg gat gtc ggt gag gca ttc gtg acc acc cag ctg   2922
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Arg Asn Pro Gly Ala Asp Val Gly Glu Ala Phe Val Thr Thr Gln Leu
        810                 815                 820
aag aag ggt tcc ggc ccc tac gtc gcg gtg tcc gac ttc gcg acc gac  2970
Lys Lys Gly Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ala Thr Asp
    825                 830                 835
ctg ccg aac cag atc cgc gag tgg gtt ccc ggt gac tac atc gtc ctc  3018
Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Ile Val Leu
840                 845                 850                 855
ggt gcc gac ggc ttc ggt ttc tcc gat acc cgt ccg gca gcc cgt cgt  3066
Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg
                860                 865                 870
tac ttc aac atc gac gcc gag tcc atc gtc gtg gcg gtc ctg cgc ggc  3114
Tyr Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Arg Gly
            875                 880                 885
ctg gtc cgc gag ggt gtc atc gat gcc tcc gtg gcg gcg cac gcg gct  3162
Leu Val Arg Glu Gly Val Ile Asp Ala Ser Val Ala Ala His Ala Ala
        890                 895                 900
gag aag tac aag ctg tcc gac ccg acg gca cca cag gtc gat ccg gac  3210
Glu Lys Tyr Lys Leu Ser Asp Pro Thr Ala Pro Gln Val Asp Pro Asp
    905                 910                 915
gca ccg atc gag tagacctgct tgtcgacgaa aaacaccccc gccccctcac      3262
Ala Pro Ile Glu
920
atgatgaggg gggcgggggt gtgctcgttt acggcgggta cagggggggta tcagcccagc 3322
atcgccttat cggagagcgt cgcgcccttg atcttggcga attcctgcag cagatcccgc 3382
acggtgagct tctgcttcac ctctgcgctg gcctcataga cgatccgtcc ctcgtgcatc 3442
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gtcagtttgc cgtcctcgac gatcttctcg gtcagggtgg tgaccagttc ggctcgctgg 3562
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<213> Corynebacterium thermoaminogenes

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Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
            20                  25                  30
Pro Glu Glu Thr Lys Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
        35                  40                  45
Asp Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
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50 55 60

Arg Ala Ser Ala Lys Arg Val Pro Leu Pro Pro Met Thr Ser Thr Asp
65 70 75 80
Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Asp Phe Pro Gly Asp
85 90 95
Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Met Arg Trp Asn Ala Ala
100 105 110
Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
115 120 125
Ile Ser Thr Tyr Ala Gly Ala Ala Pro Leu Tyr Glu Val Gly Phe Asn
130 135 140
His Phe Phe Arg Gly Lys Asp His Pro Gly Gly Gly Asp Gln Val Phe
145 150 155 160
Phe Gln Gly His Ala Ser Pro Gly Met Tyr Ala Arg Ala Phe Leu Glu
165 170 175
Gly Arg Leu Thr Glu Ser Asp Leu Asp Ser Phe Arg Gln Glu Val Ser
180 185 190
Tyr Glu Gly Gly Gly Ile Pro Ser Tyr Pro His Pro His Gly Met Pro
195 200 205
Asp Phe Trp Glu Phe Pro Thr Val Ser Met Gly Leu Gly Pro Met Asp
210 215 220
Ala Ile Tyr Gln Ala Arg Phe Asn Arg Tyr Leu His Asn Arg Gly Ile
225 230 235 240
Lys Asp Thr Ser Glu Gln His Val Trp Ala Phe Leu Gly Asp Gly Glu
245 250 255
Met Asp Glu Pro Glu Ser Arg Gly Leu Ile His Gln Ala Ala Leu Asn
260 265 270
Asn Leu Asp Asn Leu Thr Phe Val Ile Asn Cys Asn Leu Gln Arg Leu
275 280 285
Asp Gly Pro Val Arg Gly Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser
290 295 300
Phe Phe Arg Gly Ala Gly Trp Ser Val Ile Lys Val Ile Trp Gly Arg
305 310 315 320
Glu Trp Asp Glu Leu Leu Glu Lys Asp Gln Asp Gly Ala Leu Val Glu
325 330 335
Val Met Asn Asn Thr Ser Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn
340 345 350
Asp Gly Ala Tyr Val Arg Glu His Phe Phe Gly Arg Asp Pro Arg Thr
355 360 365
Leu Lys Leu Val Glu Asp Met Thr Asp Glu Glu Ile Trp Lys Leu Pro
370 375 380
Arg Gly Gly His Asp Tyr Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala
385 390 395 400

Leu Glu Thr Lys Asp Arg Pro Thr Val Ile Leu Ala His Thr Ile Lys
405 410 415
Gly Tyr Gly Leu Gly His Asn Phe Glu Gly Arg Asn Ala Thr His Gln
420 425 430
Met Lys Lys Leu Thr Leu Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln
435 440 445
Gly Leu Pro Ile Thr Asp Glu Glu Leu Glu Lys Asp Pro Tyr Leu Pro
450 455 460
Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys
465 470 475 480
Glu Arg Arg Gln Ala Leu Gly Gly Phe Leu Pro Glu Arg Arg Glu Lys
485 490 495
Tyr Glu Pro Leu Gln Val Pro Pro Leu Asp Lys Leu Arg Ser Val Arg
500 505 510
Lys Gly Ser Gly Lys Gln Gln Val Ala Thr Thr Met Ala Thr Val Arg
515 520 525
Thr Phe Lys Glu Leu Met Arg Asp Lys Asn Leu Ala Asp Arg Leu Val
530 535 540
Pro Ile Ile Pro Asp Glu Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe
545 550 555 560
Pro Thr Leu Lys Ile Tyr Asn Pro His Gly Gln Asn Tyr Val Pro Val
565 570 575
Asp His Asp Leu Met Leu Ser Tyr Arg Glu Ala Lys Asp Gly Gln Ile
580 585 590
Leu His Glu Gly Ile Asn Glu Ala Gly Ser Val Ala Ser Phe Ile Ala
595 600 605
Ala Gly Thr Ser Tyr Ala Thr His Gly Glu Ala Met Ile Pro Leu Tyr
610 615 620
Ile Phe Tyr Ser Met Phe Gly Phe Gln Arg Thr Gly Asp Gly Ile Trp
625 630 635 640
Ala Ala Ala Asp Gln Met Thr Arg Gly Phe Leu Leu Gly Ala Thr Ala
645 650 655
Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln His Met Asp Gly His
660 665 670
Ser Pro Ile Leu Ala Ser Thr Asn Pro Gly Val Glu Thr Tyr Asp Pro
675 680 685
Ala Phe Ser Tyr Glu Ile Ala His Leu Val His Arg Gly Ile Asp Arg
690 695 700
Met Tyr Gly Pro Gly Lys Gly Glu Asn Val Ile Tyr Tyr Leu Thr Ile
705 710 715 720
Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu Pro Glu Asp Leu Asp Val
725 730 735
Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr Asp Lys Ala Ala Glu Gly

740 745 750

Glu Gly His Glu Ala Ser Ile Leu Ala Ser Gly Ile Gly Met Gln Trp
755 760 765

Ala Leu Arg Ala Arg Asp Ile Leu Ala Glu Asp Tyr Gly Ile Arg Ala
770 775 780

Asn Ile Phe Ser Ala Thr Ser Trp Val Glu Leu Ala Arg Asp Gly Ala
785 790 795 800

Arg Arg Asn Leu Glu Ala Leu Arg Asn Pro Gly Ala Asp Val Gly Glu
805 810 815

Ala Phe Val Thr Thr Gln Leu Lys Lys Gly Ser Gly Pro Tyr Val Ala
820 825 830

Val Ser Asp Phe Ala Thr Asp Leu Pro Asn Gln Ile Arg Glu Trp Val
835 840 845

Pro Gly Asp Tyr Ile Val Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp
850 855 860

Thr Arg Pro Ala Ala Arg Arg Tyr Phe Asn Ile Asp Ala Glu Ser Ile
865 870 875 880

Val Val Ala Val Leu Arg Gly Leu Val Arg Glu Gly Val Ile Asp Ala
885 890 895

Ser Val Ala Ala His Ala Ala Glu Lys Tyr Lys Leu Ser Asp Pro Thr
900 905 910

Ala Pro Gln Val Asp Pro Asp Ala Pro Ile Glu
915 920

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cggcaatggg ggtctcgggc gggggggcatt ctttcacgg caaggtggtg aaatccgca 180
ggtcactccc cggccggcgg tagagaacgg agcgaaaacg gaaagcaata cgtggtttc 240
cggactggcc gttacgatgt tctgaagagt gactgccatc acccaacagg ctggtcctcg 300
tcgaaaggaa caaaaact gtg gtt aca aca aca ccc tcc acg ctg ccg gcg 351
Val Val Thr Thr Thr Pro Ser Thr Leu Pro Ala
1 5 10
ttc aaa aag atc ctg gtg gcc aac cga ggt gaa atc gcg gtg cga gca 399

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Phe Lys Lys Ile Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala
                15                  20                  25
ttc cgc gcc gcc tac gag acc ggg gcc gca acc gtg gcc atc tac ccc   447
Phe Arg Ala Ala Tyr Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro
            30                  35                  40
cgg gag gac cgt ggc tcc ttc cac cgc tcc ttc gcc tcc gag gcg gtg   495
Arg Glu Asp Arg Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val
        45                  50                  55
agg atc gga acc gag ggc tca ccc gtc aag gcg tac ctc gat att gat   543
Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp
    60                  65                  70                  75
gag atc atc aac gcc gcc aag aag gtg aaa gcg gac gcg gtc tac ccg   591
Glu Ile Ile Asn Ala Ala Lys Lys Val Lys Ala Asp Ala Val Tyr Pro
                80                  85                  90
ggg tat ggt ttc ctt tcg gaa aat gcc cag ctc gcg cgt gaa tgc gcg   639
Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala
            95                  100                 105
gag aac ggc att acc ttc atc ggt ccc acc ccg gag gtg ctc gac ctc   687
Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu
        110                 115                 120
acg ggc gac aag tcc aag gct gtg tcc gcc gcg aag aag gcc ggg ctg   735
Thr Gly Asp Lys Ser Lys Ala Val Ser Ala Ala Lys Lys Ala Gly Leu
    125                 130                 135
ccg gtg ctg gcg gaa tcc acc ccc agc acc gac atc gat gag atc gtc   783
Pro Val Leu Ala Glu Ser Thr Pro Ser Thr Asp Ile Asp Glu Ile Val
140                 145                 150                 155
aag agt gcc gag ggg cag acc tac ccg atc ttc gtc aag gcc gtc gca   831
Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala
                160                 165                 170
ggt ggt ggc ggg cgt ggt atg cgg ttc gtc gag aag ccc gag gac ctg   879
Gly Gly Gly Gly Arg Gly Met Arg Phe Val Glu Lys Pro Glu Asp Leu
            175                 180                 185
cgt gag ctg gcc agg gag gcc tcc cgc gag gcg gag gcc gct ttc ggt   927
Arg Glu Leu Ala Arg Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly
        190                 195                 200
gac gga tcc gtc tac gtc gaa cgg gcc gtg atc aaa ccc cag cac atc   975
Asp Gly Ser Val Tyr Val Glu Arg Ala Val Ile Lys Pro Gln His Ile
    205                 210                 215
gag gtg cag atc ctc ggt gat cac acc ggc gat gtc atc cac ctg tat   1023
Glu Val Gln Ile Leu Gly Asp His Thr Gly Asp Val Ile His Leu Tyr
220                 225                 230                 235
gaa cgc gac tgt tcc ctg cag cgc cgc cac cag aag gtc gtg gag atc   1071
Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile
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                    240                 245                 250
gca cct gcc cag cac ctc gac ccg gag ctg cgc gac cgc atc tgt gcc   1119
Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala
                255                 260                 265
gat gcc gtg aag ttc tgc aaa tcc atc gga tac cag ggc gcc ggc acc   1167
Asp Ala Val Lys Phe Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr
            270                 275                 280
gtg gag ttc ctc gtc gac gag gcg ggc aac cac gtc ttc att gag atg   1215
Val Glu Phe Leu Val Asp Glu Ala Gly Asn His Val Phe Ile Glu Met
        285                 290                 295
aac ccc cgc atc cag gtg gaa cac acc gtg acc gag gag gtc acc tcc   1263
Asn Pro Arg Ile Gln Val Glu His Thr Val Thr Glu Glu Val Thr Ser
300                 305                 310                 315
gtc gac ctg gtc aag gcg cag atg cac ctg gcc gcc ggt gcc acc ctg   1311
Val Asp Leu Val Lys Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu
                320                 325                 330
aag gaa ctg ggc ctg acc cag gac aag atc acc acc cac ggt gcc gcc   1359
Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala
            335                 340                 345
ctg cag tgc cgc atc acc acg gag gac ccg tcc aac aac ttc cgg ccc   1407
Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Ser Asn Asn Phe Arg Pro
        350                 355                 360
gac acc ggt gtg atc acc gcc tac cgc tcc ccg ggt ggt gcg ggt gtg   1455
Asp Thr Gly Val Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val
    365                 370                 375
cgt ctc gac ggc gca gcc cag ctc ggc ggc gag atc acc gca cat ttc   1503
Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe
380                 385                 390                 395
gat tcc atg ctg gtc aag atg acc tgc cgc ggt tcc gat ttc gag acc   1551
Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr
                400                 405                 410
gcc gtg tcc cga gcc cag cgc gcc ctg gcg gag ttc aac gtc tcc ggc   1599
Ala Val Ser Arg Ala Gln Arg Ala Leu Ala Glu Phe Asn Val Ser Gly
            415                 420                 425
gtg gcc acc aac atc ggc ttc ctg cgt gcg ctg ctg cgc gag gaa gac   1647
Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp
        430                 435                 440
ttc acc aag agg cgc atc gac acc ggc ttc atc ggc tcc cac cag cac   1695
Phe Thr Lys Arg Arg Ile Asp Thr Gly Phe Ile Gly Ser His Gln His
    445                 450                 455
ctg ctc cag gcc cca ccg gcc gac gat gag cag ggg cgg atc ctg gaa   1743
Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Glu
460                 465                 470                 475
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tac ctg gcg gat gtc acc gtg aac aaa ccc cac ggt gaa cgc ccc gag   1791
Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His Gly Glu Arg Pro Glu
                480                 485                 490
aca gcc cgt ccg ata gag aag ctg ccc gag gtg gag aac atc ccg ctg   1839
Thr Ala Arg Pro Ile Glu Lys Leu Pro Glu Val Glu Asn Ile Pro Leu
            495                 500                 505
cca cgc ggc tcc cgc gac cgc ctg aag cag ctc ggc ccg gag ggt ttc   1887
Pro Arg Gly Ser Arg Asp Arg Leu Lys Gln Leu Gly Pro Glu Gly Phe
        510                 515                 520
gcc cgc gat ctg cgc gaa cag gat gcc ctg gcc gtc acc gac acc acc   1935
Ala Arg Asp Leu Arg Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr
    525                 530                 535
ttc cgc gat gcc cac cag tcc ctc ctg gcc acc cgc gtg cgc tcc ttc   1983
Phe Arg Asp Ala His Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe
540                 545                 550                 555
gcg ctg acc ccg gcg gcg cgc gcc gtc gca aag ctc acc ccc gag ctg   2031
Ala Leu Thr Pro Ala Ala Arg Ala Val Ala Lys Leu Thr Pro Glu Leu
                560                 565                 570
ctg tcg gtg gag gcc tgg ggc ggt gcc acc tac gac gtg gcc atg cgc   2079
Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg
            575                 580                 585
ttc ctc ttc gag gat ccg tgg gca cgc ctg gat gag ctg cgt gag gcg   2127
Phe Leu Phe Glu Asp Pro Trp Ala Arg Leu Asp Glu Leu Arg Glu Ala
        590                 595                 600
atg ccg aat gtg aac atc cag atg ctg ctg cgt ggt cgc aac acc gtc   2175
Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val
    605                 610                 615
ggg tac acc ccg tac ccc gat tcg gtg tgc cgc gcg ttt gtg cag gag   2223
Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala Phe Val Gln Glu
620                 625                 630                 635
gcc gcc aag tcc ggt gtg gac atc ttc cgc atc ttc gac gcg ctc aac   2271
Ala Ala Lys Ser Gly Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn
                640                 645                 650
gac atc tcc cag atg cgc ccg gcc atc gac gcc gtc ctg gag acc ggc   2319
Asp Ile Ser Gln Met Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Gly
            655                 660                 665
acc agt gtt gcc gag gtc gcc atg gcg tac tcc ggt gac ctg tcc aat   2367
Thr Ser Val Ala Glu Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asn
        670                 675                 680
ccg ggg gag aag ctc tac acc ctg gac tac tac ctg aac ctg gcc gag   2415
Pro Gly Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu Asn Leu Ala Glu
    685                 690                 695
cag atc gtc gac tcc ggt gca cac atc ctg gcc atc aag gac atg gcc   2463
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Gln Ile Val Asp Ser Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala
700                 705                 710                 715
ggc ctg ctg cgc cgc gcc gcg gcg ccc aaa ctg gtc acc gcc ctg cgc   2511
Gly Leu Leu Arg Arg Ala Ala Ala Pro Lys Leu Val Thr Ala Leu Arg
                720                 725                 730
cgt gaa ttc gac ctg ccc gtg cat gtc cac acc cac gac acc gcc ggc   2559
Arg Glu Phe Asp Leu Pro Val His Val His Thr His Asp Thr Ala Gly
            735                 740                 745
ggt cag ctg gcc acc tac ctg gcc gcc gcc aac gcc ggg gcc gat gcc   2607
Gly Gln Leu Ala Thr Tyr Leu Ala Ala Ala Asn Ala Gly Ala Asp Ala
        750                 755                 760
gtc gac gcc gcc tcc gca ccc ctg tcc ggt acc acc tcc cag ccg tcg   2655
Val Asp Ala Ala Ser Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser
    765                 770                 775
atg tcc gct ctg gtt gcc gcg ttt gcg cac acc cga cgc gac acc ggc   2703
Met Ser Ala Leu Val Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly
780                 785                 790                 795
ctc aac ctg cag gcc gtc tcc gac ctg gaa ccg tac tgg gag gcg gtc   2751
Leu Asn Leu Gln Ala Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val
                800                 805                 810
cgc gga ctg tac ctg ccg ttt gaa tcc ggc acc ccg ggc ccg acc gga   2799
Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly
            815                 820                 825
cgc gtt tac cgc cac gag atc ccc ggc ggt cag ctg tcc aac ctg cgt   2847
Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg
        830                 835                 840
gcc cag gcc gtt gca ctg ggt ctg gcc gac cgc ttc gag ctc atc gag   2895
Ala Gln Ala Val Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu
    845                 850                 855
gac tac tac gcg gcc gtc aac gag atg ctg ggt cgt ccg acc aag gtc   2943
Asp Tyr Tyr Ala Ala Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val
860                 865                 870                 875
acc ccg tcc tcc aag gtt gtc ggt gac ctc gca ctg cac ctc gtc ggt   2991
Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly
                880                 885                 890
gcc ggt gtg agc ccg gag gat ttc gcc gcc gat ccg cag aag tac gac   3039
Ala Gly Val Ser Pro Glu Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp
            895                 900                 905
atc ccc gat tcg gtc atc gcc ttc ctc cgc ggc gaa ctg ggt acc cct   3087
Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Thr Pro
        910                 915                 920
ccc ggt ggc tgg ccc gaa ccg ctg cgc acc cgt gca ctc gag ggt cgc   3135
Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg
```

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    925                 930                 935
tcc cag ggt aag gcc ccg ctg gcg gag atc ccc gcc gag gag cag gcc   3183
Ser Gln Gly Lys Ala Pro Leu Ala Glu Ile Pro Ala Glu Glu Gln Ala
940                 945                 950                 955
cac ctg gat tcc gat gat tcc gcg gag cgt cgc ggc acc ctc aac cgc   3231
His Leu Asp Ser Asp Asp Ser Ala Glu Arg Arg Gly Thr Leu Asn Arg
                960                 965                 970
ctg ctg ttc ccg aag ccg acc gag gag ttc ctt gag cac cgt cgc cgc   3279
Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg
            975                 980                 985
ttc ggc aac acc tcc gcc ctg gat gac cgc gag ttc ttc tac ggc ttg   3327
Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu
        990                 995                1000
aag gag gga cgt gag gag ctg atc cga ctg acc ggt gtg tcc acc ccg   3375
Lys Glu Gly Arg Glu Glu Leu Ile Arg Leu Thr Gly Val Ser Thr Pro
   1005                1010                1015
atg gtg gtc cgc ctg gat gcg gtg tcc gaa ccg gat gac aaa ggc atg   3423
Met Val Val Arg Leu Asp Ala Val Ser Glu Pro Asp Asp Lys Gly Met
1020                1025                1030                1035
cgc aac gtg gtg gtc aac gtc aac ggc cag atc cgc ccg atc aag gtg   3471
Arg Asn Val Val Val Asn Val Asn Gly Gln Ile Arg Pro Ile Lys Val
                1040                1045                1050
cgc gac cgt tcc gtg gag tcc gtc acc gcc acc gcg gag aag gcc gat   3519
Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp
            1055                1060                1065
gcc acc aac aag ggc cat gtc gcc gca cca ttc gcc ggt gtg gtc acc   3567
Ala Thr Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly Val Val Thr
        1070                1075                1080
gtg acc gtc gcc gag ggt gat gag atc aag gct ggc gac gcc gtg gcc   3615
Val Thr Val Ala Glu Gly Asp Glu Ile Lys Ala Gly Asp Ala Val Ala
   1085                1090                1095
atc att gag gcc atg aag atg gag gcc acc atc acc gcg cct gtc gac   3663
Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala Pro Val Asp
1100                1105                1110                1115
ggt gtc atc gac cgc gtc gtg gtg ccc gcc gcc acc aag gtc gag ggc   3711
Gly Val Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys Val Glu Gly
                1120                1125                1130
ggc gac ctc atc gtg gtc gtg tcc tagcgactga gagccacaac ccgtcccggg   3765
Gly Asp Leu Ile Val Val Val Ser
            1135
tgccttgtta tcaacctccc cctgatgatg ttctcagggg gaggctctac gtacctcacc 3825
gtgacggtgc atgtatatcg tcctgctgga gagaatgctc caggtaggaa cgccaaccac 3885
cccactccgt gatgtcccgt gctgatccca ggcaggccgg ttggaaagaa aaaccagtga 3945
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tggaacggcc atcggacagc gagacggaac caagcgtcat cggctccggt agagcggtga 4005
ggagcctg 4013

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Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Tyr
             20                  25                  30
Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly
         35                  40                  45
Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu
     50                  55                  60
Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Asn Ala
 65                  70                  75                  80
Ala Lys Lys Val Lys Ala Asp Ala Val Tyr Pro Gly Tyr Gly Phe Leu
                 85                  90                  95
Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr
            100                 105                 110
Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser
        115                 120                 125
Lys Ala Val Ser Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu
    130                 135                 140
Ser Thr Pro Ser Thr Asp Ile Asp Glu Ile Val Lys Ser Ala Glu Gly
145                 150                 155                 160
Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg
                165                 170                 175
Gly Met Arg Phe Val Glu Lys Pro Glu Asp Leu Arg Glu Leu Ala Arg
            180                 185                 190
Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ser Val Tyr
        195                 200                 205
Val Glu Arg Ala Val Ile Lys Pro Gln His Ile Glu Val Gln Ile Leu
    210                 215                 220
Gly Asp His Thr Gly Asp Val Ile His Leu Tyr Glu Arg Asp Cys Ser
225                 230                 235                 240
Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His
                245                 250                 255
Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe
            260                 265                 270
Cys Lys Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val
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275 280 285

Asp Glu Ala Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln

290 295 300

Val Glu His Thr Val Thr Glu Glu Val Thr Ser Val Asp Leu Val Lys

305 310 315 320

Ala Gln Met His Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu

325 330 335

Thr Gln Asp Lys Ile Thr Thr His Gly Ala Ala Leu Gln Cys Arg Ile

340 345 350

Thr Thr Glu Asp Pro Ser Asn Asn Phe Arg Pro Asp Thr Gly Val Ile

355 360 365

Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala

370 375 380

Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val

385 390 395 400

Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ser Arg Ala

405 410 415

Gln Arg Ala Leu Ala Glu Phe Asn Val Ser Gly Val Ala Thr Asn Ile

420 425 430

Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Lys Arg Arg

435 440 445

Ile Asp Thr Gly Phe Ile Gly Ser His Gln His Leu Leu Gln Ala Pro

450 455 460

Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Glu Tyr Leu Ala Asp Val

465 470 475 480

Thr Val Asn Lys Pro His Gly Glu Arg Pro Glu Thr Ala Arg Pro Ile

485 490 495

Glu Lys Leu Pro Glu Val Glu Asn Ile Pro Leu Pro Arg Gly Ser Arg

500 505 510

Asp Arg Leu Lys Gln Leu Gly Pro Glu Gly Phe Ala Arg Asp Leu Arg

515 520 525

Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His

530 535 540

Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Thr Pro Ala

545 550 555 560

Ala Arg Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala

565 570 575

Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp

580 585 590

Pro Trp Ala Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn

595 600 605

Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr

610 615 620

Pro Asp Ser Val Cys Arg Ala Phe Val Gln Glu Ala Ala Lys Ser Gly
625 630 635 640
Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Ile Ser Gln Met
645 650 655
Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Gly Thr Ser Val Ala Glu
660 665 670
Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asn Pro Gly Glu Lys Leu
675 680 685
Tyr Thr Leu Asp Tyr Tyr Leu Asn Leu Ala Glu Gln Ile Val Asp Ser
690 695 700
Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Arg
705 710 715 720
Ala Ala Ala Pro Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu
725 730 735
Pro Val His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr
740 745 750
Tyr Leu Ala Ala Ala Asn Ala Gly Ala Asp Ala Val Asp Ala Ala Ser
755 760 765
Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser Met Ser Ala Leu Val
770 775 780
Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Asn Leu Gln Ala
785 790 795 800
Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu
805 810 815
Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His
820 825 830
Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Val Ala
835 840 845
Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Tyr Tyr Ala Ala
850 855 860
Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys
865 870 875 880
Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Ser Pro
885 890 895
Glu Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val
900 905 910
Ile Ala Phe Leu Arg Gly Glu Leu Gly Thr Pro Pro Gly Gly Trp Pro
915 920 925
Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Gln Gly Lys Ala
930 935 940
Pro Leu Ala Glu Ile Pro Ala Glu Glu Gln Ala His Leu Asp Ser Asp
945 950 955 960
Asp Ser Ala Glu Arg Arg Gly Thr Leu Asn Arg Leu Leu Phe Pro Lys

965 970 975
Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser
980 985 990
Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Lys Glu Gly Arg Glu
995 1000 1005
Glu Leu Ile Arg Leu Thr Gly Val Ser Thr Pro Met Val Val Arg Leu
1010 1015 1020
Asp Ala Val Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Val
025 1030 1035 1040
Asn Val Asn Gly Gln Ile Arg Pro Ile Lys Val Arg Asp Arg Ser Val
1045 1050 1055
Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp Ala Thr Asn Lys Gly
1060 1065 1070
His Val Ala Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu
1075 1080 1085
Gly Asp Glu Ile Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met
1090 1095 1100
Lys Met Glu Ala Thr Ile Thr Ala Pro Val Asp Gly Val Ile Asp Arg
105 1110 1115 1120
Val Val Val Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val
1125 1130 1135
Val Val Ser

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<213> Corynebacterium thermoaminogenes

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acc gtg aat gaa ctt ctc cgt gac gat atc cgt tat ctc ggc cgg atc 108
Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile
1 5 10 15
ctg ggc gag gtg atc tcc gag cag gag ggc cac cat gtc ttc gaa ctg 156
Leu Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu
20 25 30
gtt gaa cgc gcc cgc cgg acc tcc ttc gac atc gcc aag gga cgc gcg 204
Val Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala

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                35                  40                  45
gag atg gac agt ctg gtg gag gtg ttc gct ggc atc gac ccg gag gac   252
Glu Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp
            50                  55                  60
gcc acg ccc gtg gcc cga gcc ttc acc cat ttc gcc ctg ttg gcc aac   300
Ala Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn
        65                  70                  75
ctc gcg gag gat ttg cat gac gca gcc cag cgg gaa cag gcc ctg aac   348
Leu Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn
    80                  85                  90                  95
tcg ggt gag ccc gcg ccg gac agc acc ctc gag gcc acc tgg gtg aaa   396
Ser Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys
                100                 105                 110
ctg gat gat gcc ggg gtg ggc agc ggt gag gtc gcc gcg gtg atc cgc   444
Leu Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg
            115                 120                 125
aat gcg ctc gtc gcc ccg gtg ctc acc gcg cac ccg acg gaa acc cga   492
Asn Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg
        130                 135                 140
cgt cgt acc gtg ttc gac gcg cag aag cac atc acc gcc ctg atg gag   540
Arg Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu
    145                 150                 155
gaa cgc cac ctc ctc ctg gcg ctg ccc acg cat gcc cgg acc cag tcc   588
Glu Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser
160                 165                 170                 175
aag ctg gat gac atc gag cgc aac atc cgg cga cgg atc acg atc ctg   636
Lys Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu
                180                 185                 190
tgg cag acg gcc ctc atc cgt gtg gcc cgt ccc cgc atc gag gat gag   684
Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu
            195                 200                 205
gtc gag gtt gga ctg cgc tac tac aag ctc agc ctg ttg gcc gag atc   732
Val Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile
        210                 215                 220
ccc cgc atc aat cat gat gtg acc gtg gaa ctg gcc cgg cgt ttc ggc   780
Pro Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly
    225                 230                 235
ggg gat atc ccc acc acg gcg atg gtc agg ccg gga tcc tgg atc ggc   828
Gly Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly
240                 245                 250                 255
ggg gac cat gat ggc aac ccc ttc gtc acc gcg gag act gtc acc tac   876
Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr
                260                 265                 270
```

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gcc acc cat cgg gcc gcg gag acc gtg ctc aag tac tac gtc aag caa   924
Ala Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln
            275                 280                 285
ctg cac gcc ctg gaa cac gaa ctc agt ctc tcc gac cgg atg aac gtc   972
Leu His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val
        290                 295                 300
atc agc gat gag ctg cgt gtg ctt gcc gat gcc ggc cag aat gac atg   1020
Ile Ser Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met
    305                 310                 315
ccc agc cgg gtt gat gaa ccc tac cgg cgg gcc atc cac ggc atg cgt   1068
Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly Met Arg
320                 325                 330                 335
ggc cgg atg ctg gcc acc acg gcc gcc ctg atc ggt gag gag gcg gtc   1116
Gly Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val
                340                 345                 350
gag ggc acc tgg ttc aag acc ttc acg ccc tat acc gat acc cac gag   1164
Glu Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu
            355                 360                 365
ttc aaa cgc gac ctc gat atc gtg gat ggt tcc ctg aga atg tcc cgg   1212
Phe Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg
        370                 375                 380
gat gac atc atc gcc gat gac cgt ctg gcc atg ctg cgc tcg gcc ctg   1260
Asp Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu
    385                 390                 395
gac agc ttc ggg ttc aac ctc tac tcc ctg gat ctg cgc cag aat tcc   1308
Asp Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser
400                 405                 410                 415
gac ggt ttc gag gat gtc ctc acc gaa ttg ttc gcc acc gcc cag acc   1356
Asp Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr
                420                 425                 430
gag aag aac tac cgc ggg ttg acg gag gcg gag aag ctg gac ctg ctg   1404
Glu Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu
            435                 440                 445
atc cgc gaa ctg agc aca ccc cgc ccg ctc atc ccg cac ggg gac ccg   1452
Ile Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro
        450                 455                 460
gac tac tcc gag gcc acc aac cgt gaa ctg ggg att ttt tcg aag gcc   1500
Asp Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala
    465                 470                 475
gcg gag gcc gtg cgt aaa ttc ggt cct ctc atg gtg ccg cac tgc atc   1548
Ala Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile
480                 485                 490                 495
atc tcc atg gcc tct tcc gtc acg gac atc ctc gaa ccg atg gtg ctg   1596
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Ile Ser Met Ala Ser Ser Val Thr Asp Ile Leu Glu Pro Met Val Leu
                    500                 505                 510
ctc aag gag ttc ggt ctg atc cgg gcc aac ggg aag aac ccg acg ggc   1644
Leu Lys Glu Phe Gly Leu Ile Arg Ala Asn Gly Lys Asn Pro Thr Gly
                515                 520                 525
agc gtc gac gtg atc ccg ctg ttc gag acg atc gat gac ctc cag cgt   1692
Ser Val Asp Val Ile Pro Leu Phe Glu Thr Ile Asp Asp Leu Gln Arg
            530                 535                 540
ggc gcg ggc atc ctg gag gaa ttg tgg gac atc gac ctc tac cgc aat   1740
Gly Ala Gly Ile Leu Glu Glu Leu Trp Asp Ile Asp Leu Tyr Arg Asn
        545                 550                 555
tac ctt gag cag cgg gac aac gtc cag gag gtc atg ctg ggg tat tcc   1788
Tyr Leu Glu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser
560                 565                 570                 575
gac tcc aac aag gac ggc ggg tac ttc gcc gcc aac tgg gcg ctt tac   1836
Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp Ala Leu Tyr
                580                 585                 590
gac gcg gag tta cgc ctg gtc gaa cta tgc cgg ggc cgt aat gtc aag   1884
Asp Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly Arg Asn Val Lys
            595                 600                 605
ctc cgt ctc ttc cac ggt cgt ggt ggc acg gtg ggt cgt ggc ggt ggc   1932
Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly
        610                 615                 620
ccc tcc tat gat gcg atc ctg gcc cag ccc aag ggc gcg gtc cgg ggt   1980
Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Lys Gly Ala Val Arg Gly
    625                 630                 635
gcg gtg cgg gtg act gaa cag ggc gag atc atc tcc gcg aag tac ggt   2028
Ala Val Arg Val Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly
640                 645                 650                 655
aac ccg gat acg gca cgc cgc aac ctt gag gcc ctg gtg tcc gcg acg   2076
Asn Pro Asp Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr
                660                 665                 670
ctg gag gca tcg ctt ctg gat gat gtg gaa ctg ccc aat cgg gaa cgc   2124
Leu Glu Ala Ser Leu Leu Asp Asp Val Glu Leu Pro Asn Arg Glu Arg
            675                 680                 685
gcg cac cag atc atg ggg gag atc tcg gag ttg agc ttc cgc agg tac   2172
Ala His Gln Ile Met Gly Glu Ile Ser Glu Leu Ser Phe Arg Arg Tyr
        690                 695                 700
tca tca ctg gtc cat gag gat ccc gga ttc atc cag tac ttc acc cag   2220
Ser Ser Leu Val His Glu Asp Pro Gly Phe Ile Gln Tyr Phe Thr Gln
    705                 710                 715
tcc acc ccc ctg cag gag atc gga tcc ctc aac atc ggt tcc cga ccc   2268
Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro
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720                 725                 730                 735
tcc tca cgt aaa cag acc aac acg gtg gag gat ctg cgt gcc atc ccg   2316
Ser Ser Arg Lys Gln Thr Asn Thr Val Glu Asp Leu Arg Ala Ile Pro
                740                 745                 750
tgg gtg ctc agc tgg tcc cag tcc cgt gtc atg ctg ccg ggc tgg ttc   2364
Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe
            755                 760                 765
ggt gtg ggt acc gca ctg cgt gag tgg atc ggt gag ggg gag ggg gct   2412
Gly Val Gly Thr Ala Leu Arg Glu Trp Ile Gly Glu Gly Glu Gly Ala
        770                 775                 780
gcg gag cgc atc gcg gag ctg cag gaa ctc aac cgg tgc tgg ccg ttc   2460
Ala Glu Arg Ile Ala Glu Leu Gln Glu Leu Asn Arg Cys Trp Pro Phe
    785                 790                 795
ttc acc tcg gtg ctg gac aac atg gcc cag gtg atg agc aag gcg gaa   2508
Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu
800                 805                 810                 815
ctg cgc ctg gcc agg ttg tac gcc gat ctc atc ccg gat cgc gag gtg   2556
Leu Arg Leu Ala Arg Leu Tyr Ala Asp Leu Ile Pro Asp Arg Glu Val
                820                 825                 830
gcg gac cgg atc tat gag acc atc ttc ggg gag tat ttc ctg acc aag   2604
Ala Asp Arg Ile Tyr Glu Thr Ile Phe Gly Glu Tyr Phe Leu Thr Lys
            835                 840                 845
gag atg ttc tgc acc atc acc ggt tcc cag gac ctg ctc gat gac aac   2652
Glu Met Phe Cys Thr Ile Thr Gly Ser Gln Asp Leu Leu Asp Asp Asn
        850                 855                 860
ccg gcg ctg gcg cga tcg gtg cgc agt cgg ttc ccg tac ctg ctg ccg   2700
Pro Ala Leu Ala Arg Ser Val Arg Ser Arg Phe Pro Tyr Leu Leu Pro
    865                 870                 875
ctc aat gtc atc cag gtg gag atg atg cgc cgg tac cgg tcc ggt gat   2748
Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Ser Gly Asp
880                 885                 890                 895
gag ggc acg gct gtc cca cgt aat atc cgc ctg acc atg aat gga ttg   2796
Glu Gly Thr Ala Val Pro Arg Asn Ile Arg Leu Thr Met Asn Gly Leu
                900                 905                 910
tcc acg gcc ctg cgc aac tcg ggt tagggcgcca gacgccccgg gaacccgcac   2850
Ser Thr Ala Leu Arg Asn Ser Gly
            915
cctgtgtata ctgtctaaag ttgcccggtg tcatccgggc gtgatggata gacaacttaa 2910
cggcaaagga ttctccccac atggcactga cgcttcaaat cgtcctcgtt ctcgccagcg 2970
tgctcatgac ggtcttcgtc ctgctgcaca agggtaaggg cggaggtctg tcaagcctct 3030
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gcgtcaccat cctgaccgca gtcatctggt tgatctgcat tgtcgcgctc aacctcatcc 3150
aggcgtactc ctagcacctg atctttcaag gcctgccctt cggggcaggc ctttttgca  3210
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             20                  25                  30
Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala Glu
         35                  40                  45
Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp Ala
     50                  55                  60
Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn Leu
 65                  70                  75                  80
Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn Ser
                 85                  90                  95
Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys Leu
            100                 105                 110
Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg Asn
        115                 120                 125
Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg
    130                 135                 140
Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu Glu
145                 150                 155                 160
Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser Lys
                165                 170                 175
Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp
            180                 185                 190
Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Val
        195                 200                 205
Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile Pro
    210                 215                 220
Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly Gly
225                 230                 235                 240
Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly Gly
                245                 250                 255
Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr Ala
            260                 265                 270
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Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln Leu
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His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val Ile
290 295 300
Ser Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met Pro
305 310 315 320
Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly Met Arg Gly
325 330 335
Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val Glu
340 345 350
Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu Phe
355 360 365
Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg Asp
370 375 380
Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu Asp
385 390 395 400
Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser Asp
405 410 415
Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr Glu
420 425 430
Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu Ile
435 440 445
Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro Asp
450 455 460
Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala Ala
465 470 475 480
Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile Ile
485 490 495
Ser Met Ala Ser Ser Val Thr Asp Ile Leu Glu Pro Met Val Leu Leu
500 505 510
Lys Glu Phe Gly Leu Ile Arg Ala Asn Gly Lys Asn Pro Thr Gly Ser
515 520 525
Val Asp Val Ile Pro Leu Phe Glu Thr Ile Asp Asp Leu Gln Arg Gly
530 535 540
Ala Gly Ile Leu Glu Glu Leu Trp Asp Ile Asp Leu Tyr Arg Asn Tyr
545 550 555 560
Leu Glu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp
565 570 575
Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp Ala Leu Tyr Asp
580 585 590
Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly Arg Asn Val Lys Leu
595 600 605
Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro

610 615 620
Ser Tyr Asp Ala Ile Leu Ala Gln Pro Lys Gly Ala Val Arg Gly Ala
625 630 635 640
Val Arg Val Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn
645 650 655
Pro Asp Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu
660 665 670
Glu Ala Ser Leu Leu Asp Asp Val Glu Leu Pro Asn Arg Glu Arg Ala
675 680 685
His Gln Ile Met Gly Glu Ile Ser Glu Leu Ser Phe Arg Arg Tyr Ser
690 695 700
Ser Leu Val His Glu Asp Pro Gly Phe Ile Gln Tyr Phe Thr Gln Ser
705 710 715 720
Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser
725 730 735
Ser Arg Lys Gln Thr Asn Thr Val Glu Asp Leu Arg Ala Ile Pro Trp
740 745 750
Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly
755 760 765
Val Gly Thr Ala Leu Arg Glu Trp Ile Gly Glu Gly Glu Gly Ala Ala
770 775 780
Glu Arg Ile Ala Glu Leu Gln Glu Leu Asn Arg Cys Trp Pro Phe Phe
785 790 795 800
Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu
805 810 815
Arg Leu Ala Arg Leu Tyr Ala Asp Leu Ile Pro Asp Arg Glu Val Ala
820 825 830
Asp Arg Ile Tyr Glu Thr Ile Phe Gly Glu Tyr Phe Leu Thr Lys Glu
835 840 845
Met Phe Cys Thr Ile Thr Gly Ser Gln Asp Leu Leu Asp Asp Asn Pro
850 855 860
Ala Leu Ala Arg Ser Val Arg Ser Arg Phe Pro Tyr Leu Leu Pro Leu
865 870 875 880
Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Ser Gly Asp Glu
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Thr Ala Leu Arg Asn Ser Gly
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ttattattag ctggtggcgg agatggaact aaagctctca acgcaattca gagtgccgct 180
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gatgctaata aagaacgtaa attcttagga ttaacattaa cgcctaataa acacagatta 300
gaagaatacg ttaaatatca acaagaggat tacgaatctg atattttaga aaaacgtgaa 360
tctagacgta atcgtgaaag agaagaataa ttgaatgaaa tatctactat aatggtgggt 420
ttaaagctat caacaatttt gttgatagct atttttatgt ttcaaacata taaatattat 480
ttacttgcga ttgataacca ttctcaatta ataaaaataa cttatagtac aaatgcgtta 540
taataagttt tacttatact acctgattaa aaatgcgaaa tgaaaaatga ccccttttata 600
tacctataca gttgtgttcg aaaacatata ataatacaat ttaactaagg catataaata 660
tatagaaatt caaggggat atcaa atg gct tct aat ttt aaa gaa aca gcg 712
Met Ala Ser Asn Phe Lys Glu Thr Ala
1 5
aag aaa caa ttt gat tta aat ggc caa tca tac acg tac tat gat tta 760
Lys Lys Gln Phe Asp Leu Asn Gly Gln Ser Tyr Thr Tyr Tyr Asp Leu
10 15 20 25
aaa tca tta gaa gaa caa ggt tta act aaa att tca aag tta cct tat 808
Lys Ser Leu Glu Glu Gln Gly Leu Thr Lys Ile Ser Lys Leu Pro Tyr
30 35 40
tca atc cgt gta tta cta gaa tca gtg tta cgt cag gaa gat gat ttt 856
Ser Ile Arg Val Leu Leu Glu Ser Val Leu Arg Gln Glu Asp Asp Phe
45 50 55
gta att act gat gat cac att aaa caa tta gca gaa ttt ggc aaa aaa 904
Val Ile Thr Asp Asp His Ile Lys Gln Leu Ala Glu Phe Gly Lys Lys
60 65 70
ggt aac gaa ggt gaa gta cct ttc aaa cca tct cga gtt att tta caa 952
Gly Asn Glu Gly Glu Val Pro Phe Lys Pro Ser Arg Val Ile Leu Gln
75 80 85
gac ttc act ggt gta cca gca gta gtt gac tta gcg tct tta cgt aaa 1000
Asp Phe Thr Gly Val Pro Ala Val Val Asp Leu Ala Ser Leu Arg Lys
90 95 100 105
gca atg aat gat gtt ggt ggg gat att aat aaa att aac cct gaa gta 1048
Ala Met Asn Asp Val Gly Gly Asp Ile Asn Lys Ile Asn Pro Glu Val
110 115 120
cca gtt gac tta gtt att gac cac tct gta caa gta gat agt tat gct 1096

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Pro Val Asp Leu Val Ile Asp His Ser Val Gln Val Asp Ser Tyr Ala
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aat cca gat gca tta caa cgt aac atg aaa tta gaa ttt gaa cgt aac   1144
Asn Pro Asp Ala Leu Gln Arg Asn Met Lys Leu Glu Phe Glu Arg Asn
        140                 145                 150
tat gaa cgt tac caa ttc tta aac tgg gca aca aaa gca ttt gat aac   1192
Tyr Glu Arg Tyr Gln Phe Leu Asn Trp Ala Thr Lys Ala Phe Asp Asn
    155                 160                 165
tat aat gca gta cca cct gct aca ggt att gtc cac caa gta aac tta   1240
Tyr Asn Ala Val Pro Pro Ala Thr Gly Ile Val His Gln Val Asn Leu
170                 175                 180                 185
gaa tac tta gcg aat gtt gta cat gtt cgt gac gtt gac gga gaa caa   1288
Glu Tyr Leu Ala Asn Val Val His Val Arg Asp Val Asp Gly Glu Gln
                190                 195                 200
act gct ttc cca gat aca tta gtt ggt act gac tca cat act aca atg   1336
Thr Ala Phe Pro Asp Thr Leu Val Gly Thr Asp Ser His Thr Thr Met
            205                 210                 215
att aac ggt att ggt gta tta ggt tgg ggt gtc ggc ggt atc gaa gct   1384
Ile Asn Gly Ile Gly Val Leu Gly Trp Gly Val Gly Gly Ile Glu Ala
        220                 225                 230
gaa gca ggt atg tta gga caa cca tca tac ttc cca att cca gaa gtt   1432
Glu Ala Gly Met Leu Gly Gln Pro Ser Tyr Phe Pro Ile Pro Glu Val
    235                 240                 245
att ggt gtt aaa tta agt aat gaa tta cca caa ggt tca aca gca act   1480
Ile Gly Val Lys Leu Ser Asn Glu Leu Pro Gln Gly Ser Thr Ala Thr
250                 255                 260                 265
gac tta gca tta cgt gta act gaa gag tta cgt aaa cgt ggt gta gta   1528
Asp Leu Ala Leu Arg Val Thr Glu Glu Leu Arg Lys Arg Gly Val Val
                270                 275                 280
ggt aaa ttc gtt gag ttc ttt ggt cct ggt gta aca aac tta cca tta   1576
Gly Lys Phe Val Glu Phe Phe Gly Pro Gly Val Thr Asn Leu Pro Leu
            285                 290                 295
gct gac cgt gca aca att gcg aac atg gcg cct gaa tat ggt gca act   1624
Ala Asp Arg Ala Thr Ile Ala Asn Met Ala Pro Glu Tyr Gly Ala Thr
        300                 305                 310
tgt ggt ttc ttc cca gtt gat gaa gaa tca ctt aaa tac atg aaa tta   1672
Cys Gly Phe Phe Pro Val Asp Glu Glu Ser Leu Lys Tyr Met Lys Leu
    315                 320                 325
act ggt cgt aaa gat gat cat att gca cta gta aaa gaa tat tta caa   1720
Thr Gly Arg Lys Asp Asp His Ile Ala Leu Val Lys Glu Tyr Leu Gln
330                 335                 340                 345
caa aat aat atg ttc ttc caa gtt gaa aat gaa gat cct gaa tat act   1768
Gln Asn Asn Met Phe Phe Gln Val Glu Asn Glu Asp Pro Glu Tyr Thr
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                    350                 355                 360
gaa gtg att gat tta gat tta tct aca gtt caa gct tct tta tca ggt   1816
Glu Val Ile Asp Leu Asp Leu Ser Thr Val Gln Ala Ser Leu Ser Gly
                365                 370                 375
cca aaa cgt cca caa gat tta atc ttc tta agt gac atg aaa act gaa   1864
Pro Lys Arg Pro Gln Asp Leu Ile Phe Leu Ser Asp Met Lys Thr Glu
            380                 385                 390
ttc gaa aaa tca gtt aca gca cca gct ggt aac caa ggt cac ggt tta   1912
Phe Glu Lys Ser Val Thr Ala Pro Ala Gly Asn Gln Gly His Gly Leu
        395                 400                 405
gat gaa agt gaa ttt gat aag aaa gca gaa atc aaa ttt aat gat ggt   1960
Asp Glu Ser Glu Phe Asp Lys Lys Ala Glu Ile Lys Phe Asn Asp Gly
    410                 415                 420                 425
aga act tca act atg aag act ggt gat gtt gcg att gca gcg att aca   2008
Arg Thr Ser Thr Met Lys Thr Gly Asp Val Ala Ile Ala Ala Ile Thr
                430                 435                 440
tca tgt aca aat aca tct aac cct tac gtt atg tta ggt gca ggt tta   2056
Ser Cys Thr Asn Thr Ser Asn Pro Tyr Val Met Leu Gly Ala Gly Leu
            445                 450                 455
gta gct aaa aaa gca att gaa aaa ggc tta aaa gta cct gat tat gta   2104
Val Ala Lys Lys Ala Ile Glu Lys Gly Leu Lys Val Pro Asp Tyr Val
        460                 465                 470
aaa act tca tta gca cca ggt tca aaa gtt gtt act gga tat tta aga   2152
Lys Thr Ser Leu Ala Pro Gly Ser Lys Val Val Thr Gly Tyr Leu Arg
    475                 480                 485
gat tca ggt tta caa gaa tat ctt gat gac tta ggt ttc aac tta gtt   2200
Asp Ser Gly Leu Gln Glu Tyr Leu Asp Asp Leu Gly Phe Asn Leu Val
490                 495                 500                 505
ggt tat ggt tgt aca act tgt atc ggt aac tca ggt cca tta tta cct   2248
Gly Tyr Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Leu Pro
                510                 515                 520
gaa att gaa aaa gca gta gct gac gaa gat tta tta gta act tct gta   2296
Glu Ile Glu Lys Ala Val Ala Asp Glu Asp Leu Leu Val Thr Ser Val
            525                 530                 535
ctt tct ggt aac cgt aac ttt gaa ggt cgt atc cat ccg tta gtt aaa   2344
Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile His Pro Leu Val Lys
        540                 545                 550
gct aac tac tta gct tca cca caa tta gtt gta gct tat gca tta gct   2392
Ala Asn Tyr Leu Ala Ser Pro Gln Leu Val Val Ala Tyr Ala Leu Ala
    555                 560                 565
gga acg gtt gat atc gat tta cac aat gaa cct atc ggt aaa ggt aaa   2440
Gly Thr Val Asp Ile Asp Leu His Asn Glu Pro Ile Gly Lys Gly Lys
570                 575                 580                 585
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gat ggc gaa gat gta tac ctt aaa gat atc tgg cca agt atc aaa gaa   2488
Asp Gly Glu Asp Val Tyr Leu Lys Asp Ile Trp Pro Ser Ile Lys Glu
                590                 595                 600
gtt gca gac act gtt gat agt gtc gta acg cca gaa tta ttc tta gaa   2536
Val Ala Asp Thr Val Asp Ser Val Val Thr Pro Glu Leu Phe Leu Glu
            605                 610                 615
gaa tat gca aat gta tac gaa aat aat gaa atg tgg aat gaa atc gac   2584
Glu Tyr Ala Asn Val Tyr Glu Asn Asn Glu Met Trp Asn Glu Ile Asp
        620                 625                 630
gtt act gac gca cca tta tat gat ttc gat cca aat tca act tat att   2632
Val Thr Asp Ala Pro Leu Tyr Asp Phe Asp Pro Asn Ser Thr Tyr Ile
    635                 640                 645
caa aat cca tca ttc ttc caa ggt tta tct aaa gaa cca gga act att   2680
Gln Asn Pro Ser Phe Phe Gln Gly Leu Ser Lys Glu Pro Gly Thr Ile
650                 655                 660                 665
gaa cca tta aaa gat tta cgt att atg ggt aaa ttt ggt gat tca gtt   2728
Glu Pro Leu Lys Asp Leu Arg Ile Met Gly Lys Phe Gly Asp Ser Val
                670                 675                 680
aca act gac cac att tct cca gca ggt gcg atc ggt aaa gat aca cca   2776
Thr Thr Asp His Ile Ser Pro Ala Gly Ala Ile Gly Lys Asp Thr Pro
            685                 690                 695
gca ggt aaa tat tta tta gac cat gat gtt cca att aga gaa ttt aac   2824
Ala Gly Lys Tyr Leu Leu Asp His Asp Val Pro Ile Arg Glu Phe Asn
        700                 705                 710
tct tat ggt tca aga cgt ggt aac cat gaa gta atg gta cgt ggt act   2872
Ser Tyr Gly Ser Arg Arg Gly Asn His Glu Val Met Val Arg Gly Thr
    715                 720                 725
ttc gct aat atc cgt att aaa aac caa tta gca cca ggc act gaa ggt   2920
Phe Ala Asn Ile Arg Ile Lys Asn Gln Leu Ala Pro Gly Thr Glu Gly
730                 735                 740                 745
gga ttt aca aca tat tgg cct aca gaa gaa atc atg cct atc tat gat   2968
Gly Phe Thr Thr Tyr Trp Pro Thr Glu Glu Ile Met Pro Ile Tyr Asp
                750                 755                 760
gca gct atg aga tac aaa gaa aat ggt act ggt tta gct gtt tta gct   3016
Ala Ala Met Arg Tyr Lys Glu Asn Gly Thr Gly Leu Ala Val Leu Ala
            765                 770                 775
ggt aat gat tac ggt atg ggt tca tct cgt gac tgg gca gct aaa ggt   3064
Gly Asn Asp Tyr Gly Met Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly
        780                 785                 790
act aac tta tta ggt gtt aaa act gtt att gca caa agt tat gaa cgt   3112
Thr Asn Leu Leu Gly Val Lys Thr Val Ile Ala Gln Ser Tyr Glu Arg
    795                 800                 805
atc cat cgt tca aac tta gta atg atg ggt gta tta cca tta caa ttt   3160
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Ile His Arg Ser Asn Leu Val Met Met Gly Val Leu Pro Leu Gln Phe
810 815 820 825
aaa caa ggt gag tca gct gat tct cta ggt tta gaa ggt aaa gaa gaa 3208
Lys Gln Gly Glu Ser Ala Asp Ser Leu Gly Leu Glu Gly Lys Glu Glu
830 835 840
att tct gta gat atc gat gaa aat gtt aaa cca cat gat tta gta act 3256
Ile Ser Val Asp Ile Asp Glu Asn Val Lys Pro His Asp Leu Val Thr
845 850 855
gtt cat gct aaa aaa gaa aac gga gaa gtt gtt gat ttt gaa gca atg 3304
Val His Ala Lys Lys Glu Asn Gly Glu Val Val Asp Phe Glu Ala Met
860 865 870
gtt cgt ttc gat tca tta gta gaa tta gat tat tat cgt cat ggt ggt 3352
Val Arg Phe Asp Ser Leu Val Glu Leu Asp Tyr Tyr Arg His Gly Gly
875 880 885
atc tta caa atg gta tta aga aac aaa tta gct caa taatcacaat 3398
Ile Leu Gln Met Val Leu Arg Asn Lys Leu Ala Gln
890 895 900
gtgacttttg acagtgctaa cgtttaggtt agcactgttt ttttatgcta aactatatat 3458
gtaatgttaa tagttaagga aggattggac ttaaatgatt tatagtttga ctgaaattga 3518
accaagatat caagagacag ataaaatggg cgtgatttat catggcaatt atgcaacatg 3578
gtttgaagta gcgcgtacag attacattag aaaactagga tttagttatg ctgatatgga 3638
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35 40 45
Ser Val Leu Arg Gln Glu Asp Asp Phe Val Ile Thr Asp Asp His Ile
50 55 60
Lys Gln Leu Ala Glu Phe Gly Lys Lys Gly Asn Glu Gly Glu Val Pro
65 70 75 80

Phe Lys Pro Ser Arg Val Ile Leu Gln Asp Phe Thr Gly Val Pro Ala
85 90 95
Val Val Asp Leu Ala Ser Leu Arg Lys Ala Met Asn Asp Val Gly Gly
100 105 110
Asp Ile Asn Lys Ile Asn Pro Glu Val Pro Val Asp Leu Val Ile Asp
115 120 125
His Ser Val Gln Val Asp Ser Tyr Ala Asn Pro Asp Ala Leu Gln Arg
130 135 140
Asn Met Lys Leu Glu Phe Glu Arg Asn Tyr Glu Arg Tyr Gln Phe Leu
145 150 155 160
Asn Trp Ala Thr Lys Ala Phe Asp Asn Tyr Asn Ala Val Pro Pro Ala
165 170 175
Thr Gly Ile Val His Gln Val Asn Leu Glu Tyr Leu Ala Asn Val Val
180 185 190
His Val Arg Asp Val Asp Gly Glu Gln Thr Ala Phe Pro Asp Thr Leu
195 200 205
Val Gly Thr Asp Ser His Thr Thr Met Ile Asn Gly Ile Gly Val Leu
210 215 220
Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Gly Met Leu Gly Gln
225 230 235 240
Pro Ser Tyr Phe Pro Ile Pro Glu Val Ile Gly Val Lys Leu Ser Asn
245 250 255
Glu Leu Pro Gln Gly Ser Thr Ala Thr Asp Leu Ala Leu Arg Val Thr
260 265 270
Glu Glu Leu Arg Lys Arg Gly Val Val Gly Lys Phe Val Glu Phe Phe
275 280 285
Gly Pro Gly Val Thr Asn Leu Pro Leu Ala Asp Arg Ala Thr Ile Ala
290 295 300
Asn Met Ala Pro Glu Tyr Gly Ala Thr Cys Gly Phe Phe Pro Val Asp
305 310 315 320
Glu Glu Ser Leu Lys Tyr Met Lys Leu Thr Gly Arg Lys Asp Asp His
325 330 335
Ile Ala Leu Val Lys Glu Tyr Leu Gln Gln Asn Asn Met Phe Phe Gln
340 345 350
Val Glu Asn Glu Asp Pro Glu Tyr Thr Glu Val Ile Asp Leu Asp Leu
355 360 365
Ser Thr Val Gln Ala Ser Leu Ser Gly Pro Lys Arg Pro Gln Asp Leu
370 375 380
Ile Phe Leu Ser Asp Met Lys Thr Glu Phe Glu Lys Ser Val Thr Ala
385 390 395 400
Pro Ala Gly Asn Gln Gly His Gly Leu Asp Glu Ser Glu Phe Asp Lys
405 410 415
Lys Ala Glu Ile Lys Phe Asn Asp Gly Arg Thr Ser Thr Met Lys Thr

420 425 430

Gly Asp Val Ala Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser Asn

435 440 445

Pro Tyr Val Met Leu Gly Ala Gly Leu Val Ala Lys Lys Ala Ile Glu

450 455 460

Lys Gly Leu Lys Val Pro Asp Tyr Val Lys Thr Ser Leu Ala Pro Gly

465 470 475 480

Ser Lys Val Val Thr Gly Tyr Leu Arg Asp Ser Gly Leu Gln Glu Tyr

485 490 495

Leu Asp Asp Leu Gly Phe Asn Leu Val Gly Tyr Gly Cys Thr Thr Cys

500 505 510

Ile Gly Asn Ser Gly Pro Leu Leu Pro Glu Ile Glu Lys Ala Val Ala

515 520 525

Asp Glu Asp Leu Leu Val Thr Ser Val Leu Ser Gly Asn Arg Asn Phe

530 535 540

Glu Gly Arg Ile His Pro Leu Val Lys Ala Asn Tyr Leu Ala Ser Pro

545 550 555 560

Gln Leu Val Val Ala Tyr Ala Leu Ala Gly Thr Val Asp Ile Asp Leu

565 570 575

His Asn Glu Pro Ile Gly Lys Gly Lys Asp Gly Glu Asp Val Tyr Leu

580 585 590

Lys Asp Ile Trp Pro Ser Ile Lys Glu Val Ala Asp Thr Val Asp Ser

595 600 605

Val Val Thr Pro Glu Leu Phe Leu Glu Glu Tyr Ala Asn Val Tyr Glu

610 615 620

Asn Asn Glu Met Trp Asn Glu Ile Asp Val Thr Asp Ala Pro Leu Tyr

625 630 635 640

Asp Phe Asp Pro Asn Ser Thr Tyr Ile Gln Asn Pro Ser Phe Phe Gln

645 650 655

Gly Leu Ser Lys Glu Pro Gly Thr Ile Glu Pro Leu Lys Asp Leu Arg

660 665 670

Ile Met Gly Lys Phe Gly Asp Ser Val Thr Thr Asp His Ile Ser Pro

675 680 685

Ala Gly Ala Ile Gly Lys Asp Thr Pro Ala Gly Lys Tyr Leu Leu Asp

690 695 700

His Asp Val Pro Ile Arg Glu Phe Asn Ser Tyr Gly Ser Arg Arg Gly

705 710 715 720

Asn His Glu Val Met Val Arg Gly Thr Phe Ala Asn Ile Arg Ile Lys

725 730 735

Asn Gln Leu Ala Pro Gly Thr Glu Gly Gly Phe Thr Thr Tyr Trp Pro

740 745 750

Thr Glu Glu Ile Met Pro Ile Tyr Asp Ala Ala Met Arg Tyr Lys Glu

755 760 765

Asn Gly Thr Gly Leu Ala Val Leu Ala Gly Asn Asp Tyr Gly Met Gly
770 775 780
Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr Asn Leu Leu Gly Val Lys
785 790 795 800
Thr Val Ile Ala Gln Ser Tyr Glu Arg Ile His Arg Ser Asn Leu Val
805 810 815
Met Met Gly Val Leu Pro Leu Gln Phe Lys Gln Gly Glu Ser Ala Asp
820 825 830
Ser Leu Gly Leu Glu Gly Lys Glu Glu Ile Ser Val Asp Ile Asp Glu
835 840 845
Asn Val Lys Pro His Asp Leu Val Thr Val His Ala Lys Lys Glu Asn
850 855 860
Gly Glu Val Val Asp Phe Glu Ala Met Val Arg Phe Asp Ser Leu Val
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Glu Leu Asp Tyr Tyr Arg His Gly Gly Ile Leu Gln Met Val Leu Arg
885 890 895
Asn Lys Leu Ala Gln
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atcgccgggg agagcagcat ggtcacacgc ctgcggcgtg ccctggtgaa ggatcacggc 180
ctggacagat cgcaggtggc attcatgggt tattggaggc agggagtggc catgaggggt 240
tgatatcgct tccctgaggg tccgcaggcg tgcctcaccc tgtattcttg atagttgaac 300
aaaagagccc acataacaag gagactc atg gct aag atc atc tgg acc cgc acc 354
Met Ala Lys Ile Ile Trp Thr Arg Thr
1 5
gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag ccg gtc gtc gag 402
Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys Pro Val Val Glu
10 15 20 25
gct ttc gcc gcc acc gcg ggc atc gag gtg gag acc cgc gat atc tct 450
Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr Arg Asp Ile Ser
30 35 40

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ctc gcc ggt cgc atc ctc gca cag ttc gcg gac cag ctc ccc gag gag   498
Leu Ala Gly Arg Ile Leu Ala Gln Phe Ala Asp Gln Leu Pro Glu Glu
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cag aag gtc tcc gac gcc ctc gcc gag ctc ggc gaa ctg gct aag acc   546
Gln Lys Val Ser Asp Ala Leu Ala Glu Leu Gly Glu Leu Ala Lys Thr
            60                  65                  70
ccc gaa gcc aac atc atc aag ctt ccc aac atc tcc gca tcc gta ccg   594
Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser Ala Ser Val Pro
        75                  80                  85
cag ctc aag gct gcc gta aag gaa ctg cag gaa cag ggc tac gac ctg   642
Gln Leu Lys Ala Ala Val Lys Glu Leu Gln Glu Gln Gly Tyr Asp Leu
    90                  95                  100                 105
ccc gag tac gag gat gcc aag gac cgc tac gcc gct gtc atc ggc tcc   690
Pro Glu Tyr Glu Asp Ala Lys Asp Arg Tyr Ala Ala Val Ile Gly Ser
                110                 115                 120
aac gtc aac ccg gtc ctg cgc gag ggc aac tcc gac cgc cgc gca ccg   738
Asn Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro
            125                 130                 135
gtg gcc gtg aag aac ttc gtg aag aag ttc ccc cac cgc atg ggc gag   786
Val Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu
        140                 145                 150
tgg tcc gcc gac tcc aag acc aac gtt gcc acc atg ggt gcc gac gac   834
Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Gly Ala Asp Asp
    155                 160                 165
ttc cgc agc aat gag aag tcc gtg atc atg gac gag gcc gac acc gtg   882
Phe Arg Ser Asn Glu Lys Ser Val Ile Met Asp Glu Ala Asp Thr Val
170                 175                 180                 185
gtg atc aag cat gtc gcc gcc gac ggc acc gag acc gtg ctc aag gac   930
Val Ile Lys His Val Ala Ala Asp Gly Thr Glu Thr Val Leu Lys Asp
                190                 195                 200
agc ctc ccc ctg ctc aag ggt gag gtc atc gac ggc acc ttc atc tcc   978
Ser Leu Pro Leu Leu Lys Gly Glu Val Ile Asp Gly Thr Phe Ile Ser
            205                 210                 215
gcc aag gca ctg gac gcc ttc ctg ctc gac cag gtc aaa cgc gcc aag   1026
Ala Lys Ala Leu Asp Ala Phe Leu Leu Asp Gln Val Lys Arg Ala Lys
        220                 225                 230
gag gag ggc atc ctc ttc tcc gcc cac atg aag gcc acc atg atg aag   1074
Glu Glu Gly Ile Leu Phe Ser Ala His Met Lys Ala Thr Met Met Lys
    235                 240                 245
gtc tcc gac ccg atc atc ttc ggc cac atc gtc cgc gcc tac ttc gcc   1122
Val Ser Asp Pro Ile Ile Phe Gly His Ile Val Arg Ala Tyr Phe Ala
250                 255                 260                 265
gat gtc tac gca cag tac ggt gag cag ctg ctc gcc gcc ggc ctc aac   1170
```

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Asp Val Tyr Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly Leu Asn
                    270                 275                 280
ggt gag aac ggt ctc gcc gcc atc tac gcc ggc ctg gac aag ctg gac   1218
Gly Glu Asn Gly Leu Ala Ala Ile Tyr Ala Gly Leu Asp Lys Leu Asp
                285                 290                 295
aac ggt gcc gag atc aag gca gcc ttc gac aag ggc ctg gaa gag ggc   1266
Asn Gly Ala Glu Ile Lys Ala Ala Phe Asp Lys Gly Leu Glu Glu Gly
            300                 305                 310
ccc gac ctg gcc atg gtg aac tcc gcc aag ggc atc acc aac ctg cat   1314
Pro Asp Leu Ala Met Val Asn Ser Ala Lys Gly Ile Thr Asn Leu His
        315                 320                 325
gtg ccc tcc gat gtc atc atc gac gcc tcc atg ccc gcc atg atc cgc   1362
Val Pro Ser Asp Val Ile Ile Asp Ala Ser Met Pro Ala Met Ile Arg
330                 335                 340                 345
acc tcc ggc aag atg tgg aac aag gac gac cag acc cag gat gcc ctg   1410
Thr Ser Gly Lys Met Trp Asn Lys Asp Asp Gln Thr Gln Asp Ala Leu
                350                 355                 360
gct gtc atc ccg gac tcc tcc tac gcc ggt gtc tac cag acc gtc atc   1458
Ala Val Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr Val Ile
            365                 370                 375
gag gac tgc cgc aag aat ggc gcc ttc gat ccg acc acc atg ggc acc   1506
Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met Gly Thr
        380                 385                 390
gtc ccc aac gtc ggt ctg atg gca cag aag gcc gag gag tac ggc tcc   1554
Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr Gly Ser
    395                 400                 405
cac gac aag acc ttc cgt atc gag gcc gac ggc aag gta cag gtc gtc   1602
His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Lys Val Gln Val Val
410                 415                 420                 425
gcc tcc aac ggt gat gtc ctc atc gag cac gac gtg gag aag ggc gac   1650
Ala Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Lys Gly Asp
                430                 435                 440
atc tgg cgc gcc tgc cag acc aag gac gcc ccg atc cag gac tgg gtc   1698
Ile Trp Arg Ala Cys Gln Thr Lys Asp Ala Pro Ile Gln Asp Trp Val
            445                 450                 455
aag ctg gct gtc aac cgc gca cgt ctc tcc ggc atg ccc gct gtg ttc   1746
Lys Leu Ala Val Asn Arg Ala Arg Leu Ser Gly Met Pro Ala Val Phe
        460                 465                 470
tgg ctg gat ccc gcc cgc gca cac gac cgc aac ctg acc aca ctg gtg   1794
Trp Leu Asp Pro Ala Arg Ala His Asp Arg Asn Leu Thr Thr Leu Val
    475                 480                 485
gag aag tac ctg gca gac cac gac acc gag ggc ctg gac atc cag atc   1842
Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile
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490                 495                 500                 505
ctc tcc ccc gtc gag gcc acc cag cac gcc atc gac cgc atc cgc cgc   1890
Leu Ser Pro Val Glu Ala Thr Gln His Ala Ile Asp Arg Ile Arg Arg
                510                 515                 520
ggc gag gac acc atc tcc gtc acc ggt aac gtc ctg cgt gac tac aac   1938
Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn
            525                 530                 535
acc gac ctc ttc ccg atc ctc gag ctg ggc acc tcc gcc aag atg ctc   1986
Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu
        540                 545                 550
tcc gtc gtg cca ctg atg gcc ggc ggt gga ctc ttc gag acc ggt gcc   2034
Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala
    555                 560                 565
ggt ggc tcc gcc ccg aag cac gtc cag cag gtc atc gag gaa aac cac   2082
Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Ile Glu Glu Asn His
570                 575                 580                 585
ctg cgc tgg gat tcc ctc ggt gag ttc ctg gcc ctg gcc gag tcc ttc   2130
Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe
                590                 595                 600
cgc cac gag ctc aac acc cgc aac aac acc aag gcc ggt gtc ctc gcc   2178
Arg His Glu Leu Asn Thr Arg Asn Asn Thr Lys Ala Gly Val Leu Ala
            605                 610                 615
gat gcc ctg gac cgt gcg acc gag aag ctc ctc aac gag gag aag tcc   2226
Asp Ala Leu Asp Arg Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser
        620                 625                 630
ccg tcc cgc aag gtc ggc gag atc gac aac cgt ggt tcc cac ttc tgg   2274
Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp
    635                 640                 645
ctg gcc acc tac tgg gcc gat gaa ctg gcc aac cag acc gag gac gcc   2322
Leu Ala Thr Tyr Trp Ala Asp Glu Leu Ala Asn Gln Thr Glu Asp Ala
650                 655                 660                 665
gag ctg gct gag acc ttc gcc cct gtc gcc gag gcc ctg aac aac cag   2370
Glu Leu Ala Glu Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Asn Gln
                670                 675                 680
gct gcc gac atc gac gca gca ctc atc ggt gag cag ggc aag cct gtc   2418
Ala Ala Asp Ile Asp Ala Ala Leu Ile Gly Glu Gln Gly Lys Pro Val
            685                 690                 695
gac ctg ggt ggc tac tac gca ccc tcc gat gag aag acc tcc gcg atc   2466
Asp Leu Gly Gly Tyr Tyr Ala Pro Ser Asp Glu Lys Thr Ser Ala Ile
        700                 705                 710
atg cgc ccg gtg gcc gca ttc aac gag atc atc gac tcc ctg aag aag   2514
Met Arg Pro Val Ala Ala Phe Asn Glu Ile Ile Asp Ser Leu Lys Lys
    715                 720                 725
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taacccctc tccggagccg acagccgacg gccacgctcc cccgcccacg ggggatcgtg 2574
gccgtcggcc gtttctggca ctggagtgaa cacttcggtg ataatggtga gatgaacagc 2634
ccccgtgtcc ccgccatcct gtccgccgtt tccgccgtgg gtctgatcgc tgcgctgggc 2694
acccccgttg ccgtcgcaga caccatcacc gcggacaccg accgggaaac ctgcgtggcc 2754
agccagaatg acaactccag cgtgatcagg ttctgggatg acctggaggc cgatgtccgt 2814
gagcagcgcc tgaccgaact ggatgcacag gaccccggcc tcaagaacga catcgaggcc 2874
ttcatcgccg aggacccggt agccccctcc gcagccgatc tccagagacg gctggatgca 2934
aatgacgccg gtgagggcct ggccatgctg ctacctgaat cccgcaccga ccccgaggtg 2994
gtggacctgc ag 3006

<210> 30
<211> 729
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 30

Met	Ala	Lys	Ile	Ile	Trp	Thr	Arg	Thr	Asp	Glu	Ala	Pro	Leu	Leu	Ala
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Thr	Tyr	Ser	Leu	Lys	Pro	Val	Val	Glu	Ala	Phe	Ala	Ala	Thr	Ala	Gly
			20					25				30			
Ile	Glu	Val	Glu	Thr	Arg	Asp	Ile	Ser	Leu	Ala	Gly	Arg	Ile	Leu	Ala
		35					40					45			
Gln	Phe	Ala	Asp	Gln	Leu	Pro	Glu	Glu	Gln	Lys	Val	Ser	Asp	Ala	Leu
	50					55					60				
Ala	Glu	Leu	Gly	Glu	Leu	Ala	Lys	Thr	Pro	Glu	Ala	Asn	Ile	Ile	Lys
65					70					75					80
Leu	Pro	Asn	Ile	Ser	Ala	Ser	Val	Pro	Gln	Leu	Lys	Ala	Ala	Val	Lys
				85					90					95	
Glu	Leu	Gln	Glu	Gln	Gly	Tyr	Asp	Leu	Pro	Glu	Tyr	Glu	Asp	Ala	Lys
			100					105					110		
Asp	Arg	Tyr	Ala	Ala	Val	Ile	Gly	Ser	Asn	Val	Asn	Pro	Val	Leu	Arg
		115					120					125			
Glu	Gly	Asn	Ser	Asp	Arg	Arg	Ala	Pro	Val	Ala	Val	Lys	Asn	Phe	Val
	130					135					140				
Lys	Lys	Phe	Pro	His	Arg	Met	Gly	Glu	Trp	Ser	Ala	Asp	Ser	Lys	Thr
145					150					155					160
Asn	Val	Ala	Thr	Met	Gly	Ala	Asp	Asp	Phe	Arg	Ser	Asn	Glu	Lys	Ser
				165					170					175	
Val	Ile	Met	Asp	Glu	Ala	Asp	Thr	Val	Val	Ile	Lys	His	Val	Ala	Ala
			180					185					190		
Asp	Gly	Thr	Glu	Thr	Val	Leu	Lys	Asp	Ser	Leu	Pro	Leu	Leu	Lys	Gly
		195					200					205			
Glu	Val	Ile	Asp	Gly	Thr	Phe	Ile	Ser	Ala	Lys	Ala	Leu	Asp	Ala	Phe

210 215 220

Leu Leu Asp Gln Val Lys Arg Ala Lys Glu Glu Gly Ile Leu Phe Ser
225 230 235 240
Ala His Met Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe
245 250 255
Gly His Ile Val Arg Ala Tyr Phe Ala Asp Val Tyr Ala Gln Tyr Gly
260 265 270
Glu Gln Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala
275 280 285
Ile Tyr Ala Gly Leu Asp Lys Leu Asp Asn Gly Ala Glu Ile Lys Ala
290 295 300
Ala Phe Asp Lys Gly Leu Glu Glu Gly Pro Asp Leu Ala Met Val Asn
305 310 315 320
Ser Ala Lys Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Ile
325 330 335
Asp Ala Ser Met Pro Ala Met Ile Arg Thr Ser Gly Lys Met Trp Asn
340 345 350
Lys Asp Asp Gln Thr Gln Asp Ala Leu Ala Val Ile Pro Asp Ser Ser
355 360 365
Tyr Ala Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly
370 375 380
Ala Phe Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met
385 390 395 400
Ala Gln Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile
405 410 415
Glu Ala Asp Gly Lys Val Gln Val Val Ala Ser Asn Gly Asp Val Leu
420 425 430
Ile Glu His Asp Val Glu Lys Gly Asp Ile Trp Arg Ala Cys Gln Thr
435 440 445
Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Asn Arg Ala
450 455 460
Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Ala Arg Ala
465 470 475 480
His Asp Arg Asn Leu Thr Thr Leu Val Glu Lys Tyr Leu Ala Asp His
485 490 495
Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro Val Glu Ala Thr
500 505 510
Gln His Ala Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val
515 520 525
Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu Phe Pro Ile Leu
530 535 540
Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val Pro Leu Met Ala
545 550 555 560

Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro Lys His
565 570 575
Val Gln Gln Val Ile Glu Glu Asn His Leu Arg Trp Asp Ser Leu Gly
580 585 590
Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn Thr Arg
595 600 605
Asn Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Arg Ala Thr
610 615 620
Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val Gly Glu
625 630 635 640
Ile Asp Asn Arg Gly Ser His Phe Trp Leu Ala Thr Tyr Trp Ala Asp
645 650 655
Glu Leu Ala Asn Gln Thr Glu Asp Ala Glu Leu Ala Glu Thr Phe Ala
660 665 670
Pro Val Ala Glu Ala Leu Asn Asn Gln Ala Ala Asp Ile Asp Ala Ala
675 680 685
Leu Ile Gly Glu Gln Gly Lys Pro Val Asp Leu Gly Gly Tyr Tyr Ala
690 695 700
Pro Ser Asp Glu Lys Thr Ser Ala Ile Met Arg Pro Val Ala Ala Phe
705 710 715 720
Asn Glu Ile Ile Asp Ser Leu Lys Lys
725

<210> 31
<211> 2322
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (806)..(2212)

<400> 31
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tcataacgtc cttatgaatt tcgcagttat tagttattta aatagagaat caaactccga 120
cctagcctct gccgatgcta aaagtcagct gacccctigg ggcgcttcat ttgaaactgc 180
gaccaagctc atgaatgcgc gaaagcattt ccattataag ggtaagctgt aagaatagtg 240
ggagaaaatg ttcagtcgtg ttctaactca cttgagaaat tccatttttc tgggcttctc 300
tcaaatagat taagtggccc gtatgctgga tttctagaat atttagaagc gcgccaactc 360
atgattatgt attgtataag cctcaaagac cgaatagatt actaacattt aagtggacca 420
gagcgttaga agctttgtag agtgctcatt ccttgctgac ggcaagggtt tcctaccatg 480
agatagatcg gcagatagtt ggtttgtaaa aatttttaag gacggtccgc aatgtcaatt 540
cttgaacaga tcatcttctt catcaacacc atcttgggtt atggtctgca cgctggttct 600

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tccgcttcca gcaacctttc tcacacgatc ggcctgttct aggcctaatt ggtaataagg 660
ctgtgtaaca gtcgcccgcg tgattgtgtc ttttttaggcg cccgcgcggg cgattttcgg 720
ttttcatctt ttttaaattg agtttggaag atcaagtgcc cccggatgca cgacaatgct 780
atgccgaaca cgtattgttg aaatc gtg act gaa cat tat gac gta gta gta   832
                          Val Thr Glu His Tyr Asp Val Val Val
                            1               5
ctc gga gct ggc ccc ggt ggc tat gtc tcc gcc atc cgc gcc gcg cag   880
Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile Arg Ala Ala Gln
 10                  15                  20                  25
ctc ggt aag aaa gtt gcg gtt atc gag aag cag tac tgg gga ggt gtc   928
Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr Trp Gly Gly Val
                 30                  35                  40
tgc ctg aat gtg ggt tgt atc cca tct aag gcg ttg atc aag aac gct   976
Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Ala Leu Ile Lys Asn Ala
             45                  50                  55
gag atc gcc cac atc ttc aac cat gag aag aag acc ttc ggc atc aac  1024
Glu Ile Ala His Ile Phe Asn His Glu Lys Lys Thr Phe Gly Ile Asn
         60                  65                  70
ggc gag gtc acc ttc aac tac gag gat gcc cac aag cgt tcc cgt ggt  1072
Gly Glu Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly
     75                  80                  85
gtc tcc gac aag atc gtc ggc ggt gtt cac tac ttg atg aag aag aac  1120
Val Ser Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn
 90                  95                 100                 105
aag atc acc gag atc gac ggt ttc ggc acc ttc aag gat gcc aag acc  1168
Lys Ile Thr Glu Ile Asp Gly Phe Gly Thr Phe Lys Asp Ala Lys Thr
                110                 115                 120
atc gag gtg acc gat ggt aag gat gcc ggc aag acc gtc acc ttc gat  1216
Ile Glu Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Val Thr Phe Asp
            125                 130                 135
gac tgc atc atc gcc acc ggt tcc gtg gtc aac tcc ctc cgt ggt gtt  1264
Asp Cys Ile Ile Ala Thr Gly Ser Val Val Asn Ser Leu Arg Gly Val
        140                 145                 150
gag ttc tcc gag aac gtg gtc tcc tac gag gag cag atc ctc aac ccg  1312
Glu Phe Ser Glu Asn Val Val Ser Tyr Glu Glu Gln Ile Leu Asn Pro
    155                 160                 165
gtg gcg cct aag aag atg gtc atc gtc ggt ggc ggc gcc atc ggt atg  1360
Val Ala Pro Lys Lys Met Val Ile Val Gly Gly Gly Ala Ile Gly Met
170                 175                 180                 185
gaa ttc gcc tac gtt ctg ggc aac tac ggt gtg gac gta acc ctc atc  1408
Glu Phe Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Leu Ile
                190                 195                 200
gag ttc atg gac cgc gtt ctg ccg aac gag gat cca gag gtg tcc aag  1456
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Glu Phe Met Asp Arg Val Leu Pro Asn Glu Asp Pro Glu Val Ser Lys
                205                 210                 215
gtt atc gcc aag gcc tac aag aag atg ggc atc aag ctc ctc ccg ggc   1504
Val Ile Ala Lys Ala Tyr Lys Lys Met Gly Ile Lys Leu Leu Pro Gly
        220                 225                 230
cac gca acc acc gcg gtg cgc gac aat ggc gat tcc gtt gag gtc gat   1552
His Ala Thr Thr Ala Val Arg Asp Asn Gly Asp Ser Val Glu Val Asp
    235                 240                 245
tac cag aag aag ggc tcg gac aag acc gag acc atc acc gtc gac cgt   1600
Tyr Gln Lys Lys Gly Ser Asp Lys Thr Glu Thr Ile Thr Val Asp Arg
250                 255                 260                 265
gtt ctt atc tcc gtc ggc ttc cgc cca cgc gtc gag ggc ttc ggc ctg   1648
Val Leu Ile Ser Val Gly Phe Arg Pro Arg Val Glu Gly Phe Gly Leu
                270                 275                 280
gag aac acc ggc gtc aag ctc acc gaa cgc ggt gcc atc gac att gat   1696
Glu Asn Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Asp Ile Asp
            285                 290                 295
gag cat atg cgc acc aac gtc gac ggc atc tac gcc atc ggt gac gtc   1744
Glu His Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val
        300                 305                 310
acc gcc aag ctg cag ctg gca cac gtc gcc gag gca cag ggc att gtc   1792
Thr Ala Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val
    315                 320                 325
gcc gcc gag aca ctc gcc ggc gca gaa acc cag acc ctg ggc gac tac   1840
Ala Ala Glu Thr Leu Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr
330                 335                 340                 345
atg atg atg ccg cgt gcc acc ttc tgc aac cca cag gtt gcc tcc ttc   1888
Met Met Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ala Ser Phe
                350                 355                 360
ggt tac acc gag gag cag gcc aag gag aag tgg ccg gat cga gag atc   1936
Gly Tyr Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile
            365                 370                 375
aag gtg tcc tcc ttc ccg ttc tcc gcg aac ggc aag gcc gtc ggc ctg   1984
Lys Val Ser Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu
        380                 385                 390
gct gag acc gat ggt ttc gcc aag atc gtc gcc gac gct gag ttc ggt   2032
Ala Glu Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly
    395                 400                 405
gaa ctg ctg ggt ggc cac att gtc ggt gcc aac gcc tcc gag ctg ctc   2080
Glu Leu Leu Gly Gly His Ile Val Gly Ala Asn Ala Ser Glu Leu Leu
410                 415                 420                 425
aac gag ctg gtg ctg gcc cag aac tgg gat ctc acc acc gag gag atc   2128
Asn Glu Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile
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                  430                 435                 440
agc cgc agc gtc cac atc cac ccg acc ctg tcg gag gct gtc aag gaa   2176
Ser Arg Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu
            445                 450                 455
gct gcc cac ggc gtc aac ggc cac atg atc aac ttc taaatcccgt        2222
Ala Ala His Gly Val Asn Gly His Met Ile Asn Phe
        460                 465
cagacaaatg caaatcccct caccgatggc atatcggtga ggggatttte tcatgcacgt 2282
aaaatcataa tccatggcaa ggaaagtcga caacagcgcc                       2322
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<210> 32
<211> 469
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 32

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Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
  1               5                  10                  15
Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
            20                  25                  30
Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
        35                  40                  45
Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Asn
    50                  55                  60
His Glu Lys Lys Thr Phe Gly Ile Asn Gly Glu Val Thr Phe Asn Tyr
65                  70                  75                  80
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
                85                  90                  95
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly
            100                 105                 110
Phe Gly Thr Phe Lys Asp Ala Lys Thr Ile Glu Val Thr Asp Gly Lys
        115                 120                 125
Asp Ala Gly Lys Thr Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
    130                 135                 140
Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val
145                 150                 155                 160
Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
                165                 170                 175
Ile Val Gly Gly Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly
            180                 185                 190
Asn Tyr Gly Val Asp Val Thr Leu Ile Glu Phe Met Asp Arg Val Leu
        195                 200                 205
Pro Asn Glu Asp Pro Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
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210 215 220

Lys Met Gly Ile Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
225 230 235 240
Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
245 250 255
Lys Thr Glu Thr Ile Thr Val Asp Arg Val Leu Ile Ser Val Gly Phe
260 265 270
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu
275 280 285
Thr Glu Arg Gly Ala Ile Asp Ile Asp Glu His Met Arg Thr Asn Val
290 295 300
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala
305 310 315 320
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Leu Ala Gly
325 330 335
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr
340 345 350
Phe Cys Asn Pro Gln Val Ala Ser Phe Gly Tyr Thr Glu Glu Gln Ala
355 360 365
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ser Ser Phe Pro Phe
370 375 380
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala
385 390 395 400
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Gly His Ile
405 410 415
Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
420 425 430
Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
435 440 445
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Val Asn Gly
450 455 460
His Met Ile Asn Phe
465

<210> 33
<211> 4096
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (250)..(3951)

<400> 33

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aaagacttgt taccaaaagg tgctaatact ggggtgctag gtccccgcga ccggaaccag 180
cgttacagtg gataaaataa agcccattta gaaccctcaa caagcaagga aaagaggcga 240
gtacctgcc gtg agc agc gct agt act ttc ggc cag aac gcg tgg ctg gtg 291
          Val Ser Ser Ala Ser Thr Phe Gly Gln Asn Ala Trp Leu Val
            1               5                  10
gat gag atg ttc cag cag ttc aag aag gac ccc cag tcc gtg gac aag   339
Asp Glu Met Phe Gln Gln Phe Lys Lys Asp Pro Gln Ser Val Asp Lys
 15                  20                  25                  30
gaa tgg aga gag ctc ttc gag tct cag ggg ggt ccc cag gct gaa aag   387
Glu Trp Arg Glu Leu Phe Glu Ser Gln Gly Gly Pro Gln Ala Glu Lys
                 35                  40                  45
gct acc ccc gcc acc ccc gaa gcc aag aag gca gct tcg tcg cag tcc   435
Ala Thr Pro Ala Thr Pro Glu Ala Lys Lys Ala Ala Ser Ser Gln Ser
             50                  55                  60
tca act tcc gga cag tcc acc gcc aag gct gcc cct gcc gcc aag acc   483
Ser Thr Ser Gly Gln Ser Thr Ala Lys Ala Ala Pro Ala Ala Lys Thr
         65                  70                  75
gca ccg gcc tct gcg cca gcc aag gct gcc cct gtt aag caa aac cag   531
Ala Pro Ala Ser Ala Pro Ala Lys Ala Ala Pro Val Lys Gln Asn Gln
     80                  85                  90
gcg tcc aag cct gcc aag aag gcc aag gag tcc ccc ctg tcc aag cca   579
Ala Ser Lys Pro Ala Lys Lys Ala Lys Glu Ser Pro Leu Ser Lys Pro
 95                  100                 105                 110
gct gcc atg cct gag ccg gga acc acc cca ctc agg ggc atc ttc aag   627
Ala Ala Met Pro Glu Pro Gly Thr Thr Pro Leu Arg Gly Ile Phe Lys
                115                 120                 125
tcc atc gcc aag aac atg gac ctc tcc ctc gag gtg ccc acc gcc acc   675
Ser Ile Ala Lys Asn Met Asp Leu Ser Leu Glu Val Pro Thr Ala Thr
            130                 135                 140
tcc gtc cgc gac atg ccc gcg cgc ctc atg ttc gag aac cgc gcc atg   723
Ser Val Arg Asp Met Pro Ala Arg Leu Met Phe Glu Asn Arg Ala Met
        145                 150                 155
gtc aac gac cag ctc aag cgc acc cgt ggc ggc aag atc tcc ttc acc   771
Val Asn Asp Gln Leu Lys Arg Thr Arg Gly Gly Lys Ile Ser Phe Thr
    160                 165                 170
cac atc atc ggc tac gcc atg gtg aag gct gtc atg gca cac ccg gac   819
His Ile Ile Gly Tyr Ala Met Val Lys Ala Val Met Ala His Pro Asp
175                 180                 185                 190
atg aac aac tcc tat gac atc gtc gac ggc aag ccg tcc ctg gtc gtc   867
Met Asn Asn Ser Tyr Asp Ile Val Asp Gly Lys Pro Ser Leu Val Val
```

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                    195                 200                 205
ccg gag cac atc aac ctc ggc ctg gcc atc gac ctc ccc cag aag gac   915
Pro Glu His Ile Asn Leu Gly Leu Ala Ile Asp Leu Pro Gln Lys Asp
                210                 215                 220
ggc tcc cgt gcc ctc gtg gtc gcc gcc atc aag gaa acc gag aag atg   963
Gly Ser Arg Ala Leu Val Val Ala Ala Ile Lys Glu Thr Glu Lys Met
        225                 230                 235
acc ttc tcc cag ttc ctg gag gcc tat gag gac gtt gtg gca cgc tcc   1011
Thr Phe Ser Gln Phe Leu Glu Ala Tyr Glu Asp Val Val Ala Arg Ser
    240                 245                 250
cgc gtc ggc aag ctc acc atg gat gac tac cag ggt gtc acc atc tcc   1059
Arg Val Gly Lys Leu Thr Met Asp Asp Tyr Gln Gly Val Thr Ile Ser
255                 260                 265                 270
ttg acc aac ccg ggt ggc atc ggt acc cgc cac tcc atc ccg cgt ctg   1107
Leu Thr Asn Pro Gly Gly Ile Gly Thr Arg His Ser Ile Pro Arg Leu
                275                 280                 285
acc aag ggc cag ggc acc atc atc ggt gtc ggt tcc atg gac tac ccg   1155
Thr Lys Gly Gln Gly Thr Ile Ile Gly Val Gly Ser Met Asp Tyr Pro
            290                 295                 300
gcc gag ttc cag ggt gcc tcc gag gac cgt ctc gcc gag ctc ggt gtg   1203
Ala Glu Phe Gln Gly Ala Ser Glu Asp Arg Leu Ala Glu Leu Gly Val
        305                 310                 315
ggc aag ctc gtc acc atc acc tcc acc tac gat cac cgc gtc atc cag   1251
Gly Lys Leu Val Thr Ile Thr Ser Thr Tyr Asp His Arg Val Ile Gln
    320                 325                 330
ggc gcg gaa tcc ggt gag ttc ctg cgc acc atg tcc cag ctg ctc gtg   1299
Gly Ala Glu Ser Gly Glu Phe Leu Arg Thr Met Ser Gln Leu Leu Val
335                 340                 345                 350
gac gat gcg ttc tgg gat cac atc ttc gag gag atg aac gtt ccc tac   1347
Asp Asp Ala Phe Trp Asp His Ile Phe Glu Glu Met Asn Val Pro Tyr
                355                 360                 365
acc ccg atg cgc tgg gca cag gac ctg ccc aac acc ggt gtg gac aag   1395
Thr Pro Met Arg Trp Ala Gln Asp Leu Pro Asn Thr Gly Val Asp Lys
            370                 375                 380
aac acc cgt gtc atg cag ctc atc gag gcc tac cgc tcc cgc ggt cac   1443
Asn Thr Arg Val Met Gln Leu Ile Glu Ala Tyr Arg Ser Arg Gly His
        385                 390                 395
ctc atc gcc gac acc aac cca ctg ccc tgg gtc cag ccc ggc atg ccc   1491
Leu Ile Ala Asp Thr Asn Pro Leu Pro Trp Val Gln Pro Gly Met Pro
    400                 405                 410
gtc ccg gat cac cgt gac ctc gac atc gag acc cac ggc ctg acc ctg   1539
Val Pro Asp His Arg Asp Leu Asp Ile Glu Thr His Gly Leu Thr Leu
415                 420                 425                 430
```

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tgg gat ctg gac cgt acc ttc cac gtc ggt ggt ttc ggt ggc aag gag   1587
Trp Asp Leu Asp Arg Thr Phe His Val Gly Gly Phe Gly Gly Lys Glu
                435                 440                 445

acc atg acc ctg cgc gag gtg ctc agc cgc ctc cgc gcc gcc tac acc   1635
Thr Met Thr Leu Arg Glu Val Leu Ser Arg Leu Arg Ala Ala Tyr Thr
            450                 455                 460

ctc aag gtc ggc tcc gag tac acc cac atc ctc gac cgc gat gag cgc   1683
Leu Lys Val Gly Ser Glu Tyr Thr His Ile Leu Asp Arg Asp Glu Arg
        465                 470                 475

acc tgg ctg cag gac cgc ctc gag gcc ggt atg ccc aag ccc acc gcc   1731
Thr Trp Leu Gln Asp Arg Leu Glu Ala Gly Met Pro Lys Pro Thr Ala
    480                 485                 490

gcc gag cag aag tac atc ctg cag aag ctc aac gcc gcc gag gca ttc   1779
Ala Glu Gln Lys Tyr Ile Leu Gln Lys Leu Asn Ala Ala Glu Ala Phe
495                 500                 505                 510

gag aac ttc ctg cag acc aag tac gtc ggc cag aag cgt ttc tcc ctc   1827
Glu Asn Phe Leu Gln Thr Lys Tyr Val Gly Gln Lys Arg Phe Ser Leu
                515                 520                 525

gag ggt gcc gag tca ctg atc ccg ctg atg gac tcc gcc atc gac acc   1875
Glu Gly Ala Glu Ser Leu Ile Pro Leu Met Asp Ser Ala Ile Asp Thr
            530                 535                 540

gcc gca ggc cag ggc ctt gac gag gtc gtc atc ggc atg ccc cac cgt   1923
Ala Ala Gly Gln Gly Leu Asp Glu Val Val Ile Gly Met Pro His Arg
        545                 550                 555

ggt cgc ctc aac gtg ctg ttc aac atc gtc ggc aag cca ctg gcc tcg   1971
Gly Arg Leu Asn Val Leu Phe Asn Ile Val Gly Lys Pro Leu Ala Ser
    560                 565                 570

atc ttc aac gag ttc gag ggc cag atg gag cag ggc cag atc ggt ggc   2019
Ile Phe Asn Glu Phe Glu Gly Gln Met Glu Gln Gly Gln Ile Gly Gly
575                 580                 585                 590

tcc ggt gac gtg aag tac cac ctc ggt tcc gag ggc acc cac ctg cag   2067
Ser Gly Asp Val Lys Tyr His Leu Gly Ser Glu Gly Thr His Leu Gln
                595                 600                 605

atg ttc ggc gac ggc gag atc aag gtc tcc ctc acc gcc aac ccc tcc   2115
Met Phe Gly Asp Gly Glu Ile Lys Val Ser Leu Thr Ala Asn Pro Ser
            610                 615                 620

cac ctc gag gcc gtc aac ccg gtc gtg gag ggc atc gtc cgc gcc aag   2163
His Leu Glu Ala Val Asn Pro Val Val Glu Gly Ile Val Arg Ala Lys
        625                 630                 635

cag gac atc ctg gac aag ggc ccg gac ggc tac acc gtc gtc ccg ctg   2211
Gln Asp Ile Leu Asp Lys Gly Pro Asp Gly Tyr Thr Val Val Pro Leu
    640                 645                 650

ctg ctc cac ggt gac gcc gcc ttc gcc ggc ctg ggc atc gtg ccc gag   2259
```

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Leu Leu His Gly Asp Ala Ala Phe Ala Gly Leu Gly Ile Val Pro Glu
655                 660                 665                 670
acc atc aac ctc gca gcc ctg cgt ggt tac gat gtc ggt ggc acc atc   2307
Thr Ile Asn Leu Ala Ala Leu Arg Gly Tyr Asp Val Gly Gly Thr Ile
                675                 680                 685
cac atc gtg gtc aac aac cag atc ggc ttc acc acc acc ccg gac tcc   2355
His Ile Val Val Asn Asn Gln Ile Gly Phe Thr Thr Thr Pro Asp Ser
            690                 695                 700
agc cgt tcc atg cac tac gcc acc gac tgc gcc aag gcc ttc ggt tgc   2403
Ser Arg Ser Met His Tyr Ala Thr Asp Cys Ala Lys Ala Phe Gly Cys
        705                 710                 715
ccg gtg ttc cac gtc aac ggt gac gac ccc gag gct gtg gtc tgg gtc   2451
Pro Val Phe His Val Asn Gly Asp Asp Pro Glu Ala Val Val Trp Val
    720                 725                 730
ggc cag ctg gcc acc gag tac cgt cgc cgc ttc ggc aag gat gtc ttc   2499
Gly Gln Leu Ala Thr Glu Tyr Arg Arg Arg Phe Gly Lys Asp Val Phe
735                 740                 745                 750
atc gac ctc atc tgc tac cgc ctg cgc ggc cac aac gag gct gat gac   2547
Ile Asp Leu Ile Cys Tyr Arg Leu Arg Gly His Asn Glu Ala Asp Asp
                755                 760                 765
cca tcc atg acc cag ccg aag atg tac gag ctg atc acc ggc cgc gac   2595
Pro Ser Met Thr Gln Pro Lys Met Tyr Glu Leu Ile Thr Gly Arg Asp
            770                 775                 780
tcc gtg cgt gcc acc tac acc gag gac ctc ctc ggc cgt ggt gac ctc   2643
Ser Val Arg Ala Thr Tyr Thr Glu Asp Leu Leu Gly Arg Gly Asp Leu
        785                 790                 795
tcc ccc gag gac gcc gag gcc gtt gtc cgc gac ttc cac gac cag atg   2691
Ser Pro Glu Asp Ala Glu Ala Val Val Arg Asp Phe His Asp Gln Met
    800                 805                 810
gaa tcc gtg ttc aac gag gtc aag gaa gcc ggc aag aag cag cct gat   2739
Glu Ser Val Phe Asn Glu Val Lys Glu Ala Gly Lys Lys Gln Pro Asp
815                 820                 825                 830
gag cag acc ggc atc acc ggt tcc cag gaa ctg acc cgt ggc ctg gac   2787
Glu Gln Thr Gly Ile Thr Gly Ser Gln Glu Leu Thr Arg Gly Leu Asp
                835                 840                 845
acc aac atc acc cgc gag gaa ctg gtc gaa ctc ggc cag gcc ttc gtc   2835
Thr Asn Ile Thr Arg Glu Glu Leu Val Glu Leu Gly Gln Ala Phe Val
            850                 855                 860
aac acc cca gag ggc ttc acc tac cac cca cgt gtg gca ccg gtg gcc   2883
Asn Thr Pro Glu Gly Phe Thr Tyr His Pro Arg Val Ala Pro Val Ala
        865                 870                 875
aag aag cgt gcc gag tcc gtc acc gag ggt ggc atc gac tgg gca tgg   2931
Lys Lys Arg Ala Glu Ser Val Thr Glu Gly Gly Ile Asp Trp Ala Trp
```

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    880                 885                 890
ggc gag ctc atc gcc ttc ggc tcc ctg gcc acc tcc ggc agg ctg gtc   2979
Gly Glu Leu Ile Ala Phe Gly Ser Leu Ala Thr Ser Gly Arg Leu Val
895                 900                 905                 910
cgc ctc gcc ggt gag gat tcc cgc cgt ggt acc ttc acc cag cgt cac   3027
Arg Leu Ala Gly Glu Asp Ser Arg Arg Gly Thr Phe Thr Gln Arg His
                915                 920                 925
gcc gtg gcc atc gac ccg aac acc gcc gag gag ttc aac ccg ctc cac   3075
Ala Val Ala Ile Asp Pro Asn Thr Ala Glu Glu Phe Asn Pro Leu His
            930                 935                 940
gag ctg gca cag gcc aag ggc ggc ggc aag ttc ctc gtc tac aac tcc   3123
Glu Leu Ala Gln Ala Lys Gly Gly Gly Lys Phe Leu Val Tyr Asn Ser
        945                 950                 955
gcg ctg acc gag tac gcg ggt atg ggc ttc gaa tac ggc tac tcc gtg   3171
Ala Leu Thr Glu Tyr Ala Gly Met Gly Phe Glu Tyr Gly Tyr Ser Val
    960                 965                 970
ggc aac ccg gac gcc gtg gtg tcc tgg gag gca cag ttc ggt gac ttc   3219
Gly Asn Pro Asp Ala Val Val Ser Trp Glu Ala Gln Phe Gly Asp Phe
975                 980                 985                 990
gcc aac ggt gca cag acc atc atc gat gag tac atc tcc tcc ggt gag   3267
Ala Asn Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu
                995                1000                1005
gcc aag tgg ggc cag acc tcc tcg gtc atc ctg ctg ctg ccc cac ggt   3315
Ala Lys Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly
            1010                1015                1020
tac gag ggc cag ggt ccg gac cac tcc tcc gca cgc atc gag cgt ttc   3363
Tyr Glu Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe
        1025                1030                1035
ctg cag ctg tgc gcc gag ggt tcc atg acc atc gcc cag ccg acc acc   3411
Leu Gln Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr
    1040                1045                1050
ccg gcg aac tac ttc cac ctg ctg cgt cgt cac gca ctg ggc aag atg   3459
Pro Ala Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met
1055                1060                1065                1070
aag cgc ccg ctg gtc gtc ttc acc ccg aag tcc atg ctg cgc aac aag   3507
Lys Arg Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys
                1075                1080                1085
gcc gcc acc tcc gct ccg gag gag ttc acc gag gtc acc cgc ttc aag   3555
Ala Ala Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys
            1090                1095                1100
tcc gtg atc gac gat ccg aac gtg gcg gat gcc tcc aag gtg aag aag   3603
Ser Val Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys
        1105                1110                1115
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atc atg ctg tgc tcc ggc aag atc tac tac gaa ctg gcc aag cgc aag 3651
Ile Met Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys
1120 1125 1130
gag aag gac aac cgc gac gac atc gcg atc gtg cgc atc gag atg ctg 3699
Glu Lys Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu
1135 1140 1145 1150
cac ccg atc ccg ttc aac cgt ctg cgc gac gcc ttc gac ggc tac ccc 3747
His Pro Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro
1155 1160 1165
aac gcc gag gag atc ctg ttc gtt cag gac gag ccg gca aac cag ggt 3795
Asn Ala Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly
1170 1175 1180
gcc tgg ccg ttc tac cag gag cac ctg ccc aac ctc atc gag ggc atg 3843
Ala Trp Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met
1185 1190 1195
ctc ccg atg cgt cgc atc tcg cgc cgt tcc cag tcc tcg act gcg acc 3891
Leu Pro Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr
1200 1205 1210
ggt atc gcg aag gtg cac acc atc gag cag cag aag ctg ctg gat gat 3939
Gly Ile Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp
1215 1220 1225 1230
gcg ttc aac gca taaacgttaa tacagcggtt gatacctiga accccgccgc 3991
Ala Phe Asn Ala
accctttaga tgcgggcggg gttttgcttt gcctgcatag gcgataatat tcatatacac 4051
ccatcacgtt taagttctgc atttggatcg tgcgagcatc ccggt 4096

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Met Phe Gln Gln Phe Lys Lys Asp Pro Gln Ser Val Asp Lys Glu Trp
20 25 30
Arg Glu Leu Phe Glu Ser Gln Gly Gly Pro Gln Ala Glu Lys Ala Thr
35 40 45
Pro Ala Thr Pro Glu Ala Lys Lys Ala Ala Ser Ser Gln Ser Ser Thr
50 55 60
Ser Gly Gln Ser Thr Ala Lys Ala Ala Pro Ala Ala Lys Thr Ala Pro
65 70 75 80
Ala Ser Ala Pro Ala Lys Ala Ala Pro Val Lys Gln Asn Gln Ala Ser

Lys Pro Ala Lys Lys Ala Lys Glu Ser Pro Leu Ser Lys Pro Ala Ala
85 90 95
Met Pro Glu Pro Gly Thr Thr Pro Leu Arg Gly Ile Phe Lys Ser Ile
100 105 110
Ala Lys Asn Met Asp Leu Ser Leu Glu Val Pro Thr Ala Thr Ser Val
115 120 125
Arg Asp Met Pro Ala Arg Leu Met Phe Glu Asn Arg Ala Met Val Asn
130 135 140
Asp Gln Leu Lys Arg Thr Arg Gly Gly Lys Ile Ser Phe Thr His Ile
145 150 155 160
Ile Gly Tyr Ala Met Val Lys Ala Val Met Ala His Pro Asp Met Asn
165 170 175
Asn Ser Tyr Asp Ile Val Asp Gly Lys Pro Ser Leu Val Val Pro Glu
180 185 190
His Ile Asn Leu Gly Leu Ala Ile Asp Leu Pro Gln Lys Asp Gly Ser
195 200 205
Arg Ala Leu Val Val Ala Ala Ile Lys Glu Thr Glu Lys Met Thr Phe
210 215 220
Ser Gln Phe Leu Glu Ala Tyr Glu Asp Val Val Ala Arg Ser Arg Val
225 230 235 240
Gly Lys Leu Thr Met Asp Asp Tyr Gln Gly Val Thr Ile Ser Leu Thr
245 250 255
Asn Pro Gly Gly Ile Gly Thr Arg His Ser Ile Pro Arg Leu Thr Lys
260 265 270
Gly Gln Gly Thr Ile Ile Gly Val Gly Ser Met Asp Tyr Pro Ala Glu
275 280 285
Phe Gln Gly Ala Ser Glu Asp Arg Leu Ala Glu Leu Gly Val Gly Lys
290 295 300
Leu Val Thr Ile Thr Ser Thr Tyr Asp His Arg Val Ile Gln Gly Ala
305 310 315 320
Glu Ser Gly Glu Phe Leu Arg Thr Met Ser Gln Leu Leu Val Asp Asp
325 330 335
Ala Phe Trp Asp His Ile Phe Glu Glu Met Asn Val Pro Tyr Thr Pro
340 345 350
Met Arg Trp Ala Gln Asp Leu Pro Asn Thr Gly Val Asp Lys Asn Thr
355 360 365
Arg Val Met Gln Leu Ile Glu Ala Tyr Arg Ser Arg Gly His Leu Ile
370 375 380
Ala Asp Thr Asn Pro Leu Pro Trp Val Gln Pro Gly Met Pro Val Pro
385 390 395 400
Asp His Arg Asp Leu Asp Ile Glu Thr His Gly Leu Thr Leu Trp Asp
405 410 415
420 425 430

Leu Asp Arg Thr Phe His Val Gly Gly Phe Gly Gly Lys Glu Thr Met
435 440 445
Thr Leu Arg Glu Val Leu Ser Arg Leu Arg Ala Ala Tyr Thr Leu Lys
450 455 460
Val Gly Ser Glu Tyr Thr His Ile Leu Asp Arg Asp Glu Arg Thr Trp
465 470 475 480
Leu Gln Asp Arg Leu Glu Ala Gly Met Pro Lys Pro Thr Ala Ala Glu
485 490 495
Gln Lys Tyr Ile Leu Gln Lys Leu Asn Ala Ala Glu Ala Phe Glu Asn
500 505 510
Phe Leu Gln Thr Lys Tyr Val Gly Gln Lys Arg Phe Ser Leu Glu Gly
515 520 525
Ala Glu Ser Leu Ile Pro Leu Met Asp Ser Ala Ile Asp Thr Ala Ala
530 535 540
Gly Gln Gly Leu Asp Glu Val Val Ile Gly Met Pro His Arg Gly Arg
545 550 555 560
Leu Asn Val Leu Phe Asn Ile Val Gly Lys Pro Leu Ala Ser Ile Phe
565 570 575
Asn Glu Phe Glu Gly Gln Met Glu Gln Gly Gln Ile Gly Gly Ser Gly
580 585 590
Asp Val Lys Tyr His Leu Gly Ser Glu Gly Thr His Leu Gln Met Phe
595 600 605
Gly Asp Gly Glu Ile Lys Val Ser Leu Thr Ala Asn Pro Ser His Leu
610 615 620
Glu Ala Val Asn Pro Val Val Glu Gly Ile Val Arg Ala Lys Gln Asp
625 630 635 640
Ile Leu Asp Lys Gly Pro Asp Gly Tyr Thr Val Val Pro Leu Leu Leu
645 650 655
His Gly Asp Ala Ala Phe Ala Gly Leu Gly Ile Val Pro Glu Thr Ile
660 665 670
Asn Leu Ala Ala Leu Arg Gly Tyr Asp Val Gly Gly Thr Ile His Ile
675 680 685
Val Val Asn Asn Gln Ile Gly Phe Thr Thr Thr Pro Asp Ser Ser Arg
690 695 700
Ser Met His Tyr Ala Thr Asp Cys Ala Lys Ala Phe Gly Cys Pro Val
705 710 715 720
Phe His Val Asn Gly Asp Asp Pro Glu Ala Val Val Trp Val Gly Gln
725 730 735
Leu Ala Thr Glu Tyr Arg Arg Arg Phe Gly Lys Asp Val Phe Ile Asp
740 745 750
Leu Ile Cys Tyr Arg Leu Arg Gly His Asn Glu Ala Asp Asp Pro Ser
755 760 765
Met Thr Gln Pro Lys Met Tyr Glu Leu Ile Thr Gly Arg Asp Ser Val

770 775 780

Arg Ala Thr Tyr Thr Glu Asp Leu Leu Gly Arg Gly Asp Leu Ser Pro
785 790 795 800
Glu Asp Ala Glu Ala Val Val Arg Asp Phe His Asp Gln Met Glu Ser
805 810 815
Val Phe Asn Glu Val Lys Glu Ala Gly Lys Lys Gln Pro Asp Glu Gln
820 825 830
Thr Gly Ile Thr Gly Ser Gln Glu Leu Thr Arg Gly Leu Asp Thr Asn
835 840 845
Ile Thr Arg Glu Glu Leu Val Glu Leu Gly Gln Ala Phe Val Asn Thr
850 855 860
Pro Glu Gly Phe Thr Tyr His Pro Arg Val Ala Pro Val Ala Lys Lys
865 870 875 880
Arg Ala Glu Ser Val Thr Glu Gly Gly Ile Asp Trp Ala Trp Gly Glu
885 890 895
Leu Ile Ala Phe Gly Ser Leu Ala Thr Ser Gly Arg Leu Val Arg Leu
900 905 910
Ala Gly Glu Asp Ser Arg Arg Gly Thr Phe Thr Gln Arg His Ala Val
915 920 925
Ala Ile Asp Pro Asn Thr Ala Glu Glu Phe Asn Pro Leu His Glu Leu
930 935 940
Ala Gln Ala Lys Gly Gly Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu
945 950 955 960
Thr Glu Tyr Ala Gly Met Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn
965 970 975
Pro Asp Ala Val Val Ser Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn
980 985 990
Gly Ala Gln Thr Ile Ile Asp Glu Tyr Ile Ser Ser Gly Glu Ala Lys
995 1000 1005
Trp Gly Gln Thr Ser Ser Val Ile Leu Leu Leu Pro His Gly Tyr Glu
1010 1015 1020
Gly Gln Gly Pro Asp His Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln
025 1030 1035 1040
Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr Thr Pro Ala
1045 1050 1055
Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly Lys Met Lys Arg
1060 1065 1070
Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu Arg Asn Lys Ala Ala
1075 1080 1085
Thr Ser Ala Pro Glu Glu Phe Thr Glu Val Thr Arg Phe Lys Ser Val
1090 1095 1100
Ile Asp Asp Pro Asn Val Ala Asp Ala Ser Lys Val Lys Lys Ile Met
105 1110 1115 1120

Leu Cys Ser Gly Lys Ile Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys
1125 1130 1135
Asp Asn Arg Asp Asp Ile Ala Ile Val Arg Ile Glu Met Leu His Pro
1140 1145 1150
Ile Pro Phe Asn Arg Leu Arg Asp Ala Phe Asp Gly Tyr Pro Asn Ala
1155 1160 1165
Glu Glu Ile Leu Phe Val Gln Asp Glu Pro Ala Asn Gln Gly Ala Trp
1170 1175 1180
Pro Phe Tyr Gln Glu His Leu Pro Asn Leu Ile Glu Gly Met Leu Pro
185 1190 1195 1200
Met Arg Arg Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr Gly Ile
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Ala Lys Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp Ala Phe
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Asn Ala

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<212> DNA
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<220>
<223> Description of Artificial Sequence: primer for aceA

<400> 35
cctctaccca gcgaactccg 20

<210> 36
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<400> 36
ctgccttgaa ctcacggttc 20

<210> 37
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<212> DNA
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<220>
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<400> 37
catccacccc ggctacggct 20

<210> 38
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<212> DNA
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<220>
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<400> 38
cggtgactgg gtgttccacc 20

<210> 39
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<220>
<223> Description of Artificial Sequence: primer for dtsRI

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<210> 40
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<220>
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<400> 40
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<210> 41
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<220>
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<400> 42
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<210> 43
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<220>
<223> Description of Artificial Sequence: primer for pfk

<400> 43
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<210> 44
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<220>
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<400> 44
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<210> 45
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for scrB

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<223> n=a or g or c or t

<400> 45
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<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for scrB

<220>
<221> UNSURE
<222> (18)
<223> n=a or g or c or t

<400> 46
ggrcaytccc acatrtancc 20

<210> 47
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer for gluABCD

<400> 47
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<210> 48
<211> 20
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for gluABCD

<400> 48
aatcccatct cgtgggtaac 20

<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for pdhA

<400> 49
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<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for pdhA

<400> 50
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<210> 51
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for pc

<400> 51
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<210> 52
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for pc

<400> 52
tggccgcctg ggatctcgtg 20

<210> 53
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for ppc

<400> 53
ggttcctgga ttggtggaga 20

<210> 54
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for ppc

<400> 54
ccgccatcct tgttggaatc 20

<210> 55
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for acn

<220>
<221> UNSURE
<222> (3,6,9)
<223> n=inosine

<400> 55
gtnggnacng aytcscatac 20

<210> 56
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for acn

<220>
<221> UNSURE
<222> (3,9,18)
<223> n=inosine

<400> 56
gcnggagana tgtgrtcngt 20

<210> 57
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for icd

<400> 57
gacatttcac tcgctggacg 20

<210> 58
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for icd

<400> 58
ccgtactctt cagccttctg 20

<210> 59

<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for lpd

<400> 59
atcatcgcaa ccggttc 17

<210> 60
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for lpd

<400> 60
cgtcaccgat ggcgtaaat 19

<210> 61
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for odhA

<400> 61
acaccgtggt cgcctcaacg 20

<210> 62
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for odhA

<400> 62
tgctaacccg tcccacctgg 20

<210> 63
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for screening PCR of lpd

<400> 63
tacgaggagc agatcctcaa 20

<210> 64
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for screening PCR of lpd

<400> 64
ttgacgccgg tgttctccag 20

<210> 65
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for LA cloning of acn

<400> 65
ggtgaagcta agtagttagc 20

<210> 66
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for

LA cloning of acn

<400> 66
agctactaaa cctgcacc 18

<210> 67
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 67
ccgtactctt cagccttctg 67

<210> 68
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 68
tcgtccttgt tccacatc 18

<210> 69
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of lpd

<400> 69
atcatcgcaa ccggttc 17

<210> 70
<211> 20

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of lpd

<400> 70
tacgaggagc agatcctcaa 20

<210> 71
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of acn

<400> 71
gctaactact tagcttcacc 20

<210> 72
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of acn

<400> 72
gaaccaggaa ctattgaacc 20

<210> 73
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 73
tccgatgtca tcatcgac 18

<210> 74
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of icd

<400> 74
atgtggaaca aggacgac 18

<210> 75
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of odhA

<400> 75
gtacatattg tcgttagaac gcgtaatacg actca 35

<210> 76
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for
LA cloning of odhA

<400> 76
cgttagaacg cgtaatacga ctcactatag ggaga 35

<210> 77
<211> 32
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying gdh gene

<400> 77
gcgcctgcag gtccgagggt gtgcgttcgg ca 32

<210> 78
<211> 32
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying gdh gene

<400> 78
gcgcctgcag ccaccagga tgccctcaacc ag 32

<210> 79
<211> 1344
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (1)..(1341)

<400> 79
atg act gta gat gag cag gtc tcc aac tac tac gac atg ctg ctg aag 48
Met Thr Val Asp Glu Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys
1 5 10 15
cgc aac gcc ggg gaa cct gag ttc cac cag gct gtc gcg gag gtt ctc 96
Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
20 25 30
gaa tct ctg aag atc gtc ctg gag aag gac ccg cac tac gcc gac tac 144
Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
35 40 45
ggt ctg atc cag cgt ctc tgc gaa ccg gaa cgc cag ctg atc ttc cgt 192

```
Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
     50                  55                  60
gtg ccc tgg gtg gat gac aac ggt cag gtg cac gtc aac cgt ggt ttc   240
Val Pro Trp Val Asp Asp Asn Gly Gln Val His Val Asn Arg Gly Phe
 65                  70                  75                  80
cgt gtc cag ttc aac tcc gca ctc ggc ccg tac aag ggt ggt ctg cgt   288
Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
                 85                  90                  95
ttc cac ccc tcc gtc aac ctc ggc atc gtc aag ttc ctc ggc ttc gag   336
Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu
            100                 105                 110
cag atc ttc aag aac tcc ctc acc ggt ctg ccg atc ggt ggc ggc aag   384
Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
        115                 120                 125
ggt ggt tcc gac ttc gac ccg aag ggc aag tcc gag ctg gag atc atg   432
Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Leu Glu Ile Met
    130                 135                 140
cgc ttc tgc cag tcc ttc atg acc gag ctg cac cgc cac atc ggc gag   480
Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu
145                 150                 155                 160
tac cgg gat gtc ccg gcc ggt gac atc gga gtc ggt ggc cgc gag atc   528
Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile
                165                 170                 175
ggt tac ctc ttc ggc cac tac cgc cgt ctg gcc aac cag cac gag tcc   576
Gly Tyr Leu Phe Gly His Tyr Arg Arg Leu Ala Asn Gln His Glu Ser
            180                 185                 190
ggt gtg ctc acc ggc aag ggc ctg acc tgg ggt ggt tcc ctg gtc cgc   624
Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg
        195                 200                 205
acc gag gcc acc ggc ttc ggc acc gtc tac ttc gtc cag gag atg atc   672
Thr Glu Ala Thr Gly Phe Gly Thr Val Tyr Phe Val Gln Glu Met Ile
    210                 215                 220
aag gcg gaa ggg gag acc ctc gag ggc aag aag gtc atc gtc tcc ggt   720
Lys Ala Glu Gly Glu Thr Leu Glu Gly Lys Lys Val Ile Val Ser Gly
225                 230                 235                 240
tcc ggc aac gtg gcc acc tac gcc atc cag aag gtg cag gaa ctg ggt   768
Ser Gly Asn Val Ala Thr Tyr Ala Ile Gln Lys Val Gln Glu Leu Gly
                245                 250                 255
gcg gtt gtg gtc ggc ttc tcc gac tcc agc ggc tgg gtc tcc acc ccg   816
Ala Val Val Val Gly Phe Ser Asp Ser Ser Gly Trp Val Ser Thr Pro
            260                 265                 270
aac ggt gtt gac gtg gcc aag ctg cgt gag atc aag gag gtc cgt cgt   864
Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg
```

```
          275                 280                 285
gca cgc gtg tcc tcc tac gcc gac gag gtg gag ggt gcg gag tac cac   912
Ala Arg Val Ser Ser Tyr Ala Asp Glu Val Glu Gly Ala Glu Tyr His
    290                 295                 300
acc gac ggc tcc atc tgg gat ctg acc gcc gac atc gcg ctg ccc tgc   960
Thr Asp Gly Ser Ile Trp Asp Leu Thr Ala Asp Ile Ala Leu Pro Cys
305                 310                 315                 320
gcc acc cag aac gaa ctg gac ggc gac aac gcc cgc acc ctc gcg gac  1008
Ala Thr Gln Asn Glu Leu Asp Gly Asp Asn Ala Arg Thr Leu Ala Asp
                325                 330                 335
aac ggc tgc cgc ttc gtg gcg gag ggc gcc aac atg ccc tcc acc ccc  1056
Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
            340                 345                 350
gag gcc atc gac gtc ttc cgt gag cgt ggt gtt ctc ttc ggg ccg ggc  1104
Glu Ala Ile Asp Val Phe Arg Glu Arg Gly Val Leu Phe Gly Pro Gly
        355                 360                 365
aag gct gcc aac gcc ggt ggc gtg gcc acc tcc gcc ctg gag atg cag  1152
Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
    370                 375                 380
cag aac gcc tcc cgt gat tcc tgg agc ttc gag tac acc gat gag cgt  1200
Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
385                 390                 395                 400
ctc cac cgc atc atg aag aac atc ttc aag tcc tgc gcc gat acc gcc  1248
Leu His Arg Ile Met Lys Asn Ile Phe Lys Ser Cys Ala Asp Thr Ala
                405                 410                 415
aag gag tac ggc cac gag aag aac tac gtg gtc ggt gcg aac atc gcc  1296
Lys Glu Tyr Gly His Glu Lys Asn Tyr Val Val Gly Ala Asn Ile Ala
            420                 425                 430
gga ttc aag aag gtc gct gac gcc atg ctc gcc cag ggt gtc atc taa  1344
Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
        435                 440                 445
```

<210> 80
<211> 447
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 80

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Met Thr Val Asp Glu Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys
  1               5                  10                  15
Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
            20                  25                  30
Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
```

35 40 45

Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
50 55 60
Val Pro Trp Val Asp Asp Asn Gly Gln Val His Val Asn Arg Gly Phe
65 70 75 80
Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
85 90 95
Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu
100 105 110
Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
115 120 125
Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Leu Glu Ile Met
130 135 140
Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu
145 150 155 160
Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile
165 170 175
Gly Tyr Leu Phe Gly His Tyr Arg Arg Leu Ala Asn Gln His Glu Ser
180 185 190
Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg
195 200 205
Thr Glu Ala Thr Gly Phe Gly Thr Val Tyr Phe Val Gln Glu Met Ile
210 215 220
Lys Ala Glu Gly Glu Thr Leu Glu Gly Lys Lys Val Ile Val Ser Gly
225 230 235 240
Ser Gly Asn Val Ala Thr Tyr Ala Ile Gln Lys Val Gln Glu Leu Gly
245 250 255
Ala Val Val Val Gly Phe Ser Asp Ser Ser Gly Trp Val Ser Thr Pro
260 265 270
Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg
275 280 285
Ala Arg Val Ser Ser Tyr Ala Asp Glu Val Glu Gly Ala Glu Tyr His
290 295 300
Thr Asp Gly Ser Ile Trp Asp Leu Thr Ala Asp Ile Ala Leu Pro Cys
305 310 315 320
Ala Thr Gln Asn Glu Leu Asp Gly Asp Asn Ala Arg Thr Leu Ala Asp
325 330 335
Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
340 345 350
Glu Ala Ile Asp Val Phe Arg Glu Arg Gly Val Leu Phe Gly Pro Gly
355 360 365
Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
370 375 380

```
Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
385                 390                 395                 400
Leu His Arg Ile Met Lys Asn Ile Phe Lys Ser Cys Ala Asp Thr Ala
                405                 410                 415
Lys Glu Tyr Gly His Glu Lys Asn Tyr Val Val Gly Ala Asn Ile Ala
            420                 425                 430
Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
        435                 440                 445
```

<210> 81
<211> 1344
<212> DNA
<213> Brevibacterium lactofermentum

<220>
<221> CDS
<222> (1)..(1341)

<400> 81

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atg aca gtt gat gag cag gtc tct aac tat tac gac atg ctt ctg aag   48
Met Thr Val Asp Glu Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys
 1               5                  10                  15
cgc aat gct ggc gag cct gaa ttt cac cag gca gtg gca gag gtt ttg   96
Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
            20                  25                  30
gaa tct ttg aag atc gtc ctg gaa aag gac cct cat tac gct gat tac  144
Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
        35                  40                  45
ggt ctc atc cag cgc ctg tgc gag cct gag cgt cag ctc atc ttc cgt  192
Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
    50                  55                  60
gtg cct tgg gtt gat gac cag ggc cag gtc cac gtc aac cgt ggt ttc  240
Val Pro Trp Val Asp Asp Gln Gly Gln Val His Val Asn Arg Gly Phe
65                  70                  75                  80
cgc gtg cag ttc aac tct gca ctt gga cca tac aag ggc ggc ctg cgc  288
Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
                85                  90                  95
ttc cac cca tct gta aac ctg ggc att gtg aag ttc ctg ggc ttt gag  336
Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu
            100                 105                 110
cag atc ttt aaa aac tcc cta acc ggc ctg cca atc ggt ggt ggc aag  384
Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
        115                 120                 125
```

```
ggt gga tcc gac ttc gac cct aag ggc aag tcc gat ctg gaa atc atg   432
Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met
    130                 135                 140
cgt ttc tgc cag tcc ttc atg acc gag ctg cac cgc cac atc ggt gag   480
Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu
145                 150                 155                 160
tac cgc gac gtt cct gca ggt gac atc gga gtt ggt ggc cgc gag atc   528
Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile
                165                 170                 175
ggt tac ctg ttt ggc cac tac cgt cgc atg gct aac cag cac gag tcc   576
Gly Tyr Leu Phe Gly His Tyr Arg Arg Met Ala Asn Gln His Glu Ser
            180                 185                 190
ggc gtt ttg acc ggt aag ggc ctg acc tgg ggt gga tcc ctg gtc cgc   624
Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg
        195                 200                 205
acc gag gca act ggc tac ggc tgc gtt tac ttc gtg agt gaa atg atc   672
Thr Glu Ala Thr Gly Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile
    210                 215                 220
aag gct aag ggc gag agc atc agc ggc cag aag atc atc gtt tcc ggt   720
Lys Ala Lys Gly Glu Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly
225                 230                 235                 240
tcc ggc aac gta gca acc tac gcg att gaa aag gct cag gaa ctc ggc   768
Ser Gly Asn Val Ala Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly
                245                 250                 255
gca acc gtt att ggt ttc tcc gat tcc agc ggt tgg gtt cat acc cct   816
Ala Thr Val Ile Gly Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro
            260                 265                 270
aac ggc gtt gac gtg gct aag ctc cgc gaa atc aag gaa gtt cgc cgc   864
Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg
        275                 280                 285
gca cgc gta tcc gtg tac gcc gac gaa att gaa ggc gca acc tac cac   912
Ala Arg Val Ser Val Tyr Ala Asp Glu Ile Glu Gly Ala Thr Tyr His
    290                 295                 300
acc gac ggt tcc atc tgg gat ctc aag tgc gat atc gct ctt cct tgt   960
Thr Asp Gly Ser Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys
305                 310                 315                 320
gca act cag aac gag ctc aac ggc gag aac gct aag act ctt gca gac  1008
Ala Thr Gln Asn Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp
                325                 330                 335
aac ggc tgc cgt ttc gtt gct gaa ggc gcg aac atg cct tcc acc cct  1056
Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
            340                 345                 350
gag gct gtt gag gtc ttc cgt gag cgc gac atc cgc ttc gga cca ggc  1104
```

```
Glu Ala Val Glu Val Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly
        355                 360                 365
aag gca gct aac gct ggt ggc gtt gca acc tcc gct ctg gag atg cag   1152
Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
    370                 375                 380
cag aac gct tcg cgc gat tcc tgg agc ttc gag tac acc gac gag cgc   1200
Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
385                 390                 395                 400
ctc cag gtg atc atg aag aac atc ttc aag acc tgt gca gag acc gca   1248
Leu Gln Val Ile Met Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala
                405                 410                 415
gca gag tat gga cac gag aac gat tac gtt gtc ggc gct aac att gct   1296
Ala Glu Tyr Gly His Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala
            420                 425                 430
ggc ttt aag aag gta gct gac gcg atg ctg gca cag ggc gtc atc taa   1344
Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
        435                 440                 445
```

<210> 82
<211> 447
<212> PRT
<213> Brevibacterium lactofermentum

<400> 82

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Met Thr Val Asp Glu Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys
 1               5                  10                  15
Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
            20                  25                  30
Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
        35                  40                  45
Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
    50                  55                  60
Val Pro Trp Val Asp Asp Gln Gly Gln Val His Val Asn Arg Gly Phe
65                  70                  75                  80
Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
                85                  90                  95
Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu
            100                 105                 110
Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
        115                 120                 125
Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met
    130                 135                 140
Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu
```

145 150 155 160
Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile
165 170 175
Gly Tyr Leu Phe Gly His Tyr Arg Arg Met Ala Asn Gln His Glu Ser
180 185 190
Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg
195 200 205
Thr Glu Ala Thr Gly Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile
210 215 220
Lys Ala Lys Gly Glu Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly
225 230 235 240
Ser Gly Asn Val Ala Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly
245 250 255
Ala Thr Val Ile Gly Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro
260 265 270
Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg
275 280 285
Ala Arg Val Ser Val Tyr Ala Asp Glu Ile Glu Gly Ala Thr Tyr His
290 295 300
Thr Asp Gly Ser Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys
305 310 315 320
Ala Thr Gln Asn Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp
325 330 335
Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
340 345 350
Glu Ala Val Glu Val Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly
355 360 365
Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
370 375 380
Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
385 390 395 400
Leu Gln Val Ile Met Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala
405 410 415
Ala Glu Tyr Gly His Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala
420 425 430
Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
435 440 445

<210> 83
<211> 20
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying gltA gene

<220>
<221> misc_feature
<222> (9)
<223> n=inosine

<400> 83
aagatcacnt acatcgaygg 20

<210> 84
<211> 20
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying gltA gene

<400> 84
tagaagtcta cgttcgggta 20

<210> 85
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying gltA gene

<400> 85
gtcgacaata gcctgaatct g 21

<210> 86
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying gltA gene

<400> 86
cggtggaacc ggtgctgaca t 21

<210> 87
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying gltA gene

<400> 87
gggtgggga attcggtcatg t 21

<210> 88
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying gltA gene

<400> 88
tgtcgtagcc gcggtagcgc a 21

<210> 89
<211> 1293
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (1)..(1290)

<400> 89

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gtg gct tct gat aac aac aag gct gta ctg cac tac cct ggc ggc gaa   48
Val Ala Ser Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu
 1               5                  10                  15
ttc gag atg ggc atc aag cag gcc acc gag ggt aac tcc ggt gtc atc   96
Phe Glu Met Gly Ile Lys Gln Ala Thr Glu Gly Asn Ser Gly Val Ile
            20                  25                  30
ctg ggt aag atg ctg tcg gaa acc ggt ctg gtc acc ttc gac ccc ggt  144
Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly
        35                  40                  45
tat gtc agc acc ggt tcc acc gaa tcc aag atc acc tac atc gat ggt  192
Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly
    50                  55                  60
gat gca ggc atc ctg cgc tac cgc ggc tac gac att gcg gat ctg gcc  240
Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala
65                  70                  75                  80
gaa aat gcc acc ttc aat gag gtc tcc tac ctc ctg atc aag ggt gag  288
Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Lys Gly Glu
                85                  90                  95
ctc ccg acc ccg gaa gag ctc cac aag ttc aac gac gag att cgt cac  336
Leu Pro Thr Pro Glu Glu Leu His Lys Phe Asn Asp Glu Ile Arg His
            100                 105                 110
cac acc ctg ctg gac gag gac ttc aag tcc cag ttc aat gtc ttc cct  384
His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro
        115                 120                 125
cgc gat gcc cac ccg atg gcc acc ctg gcc tcc tcg gtt aac atc ctc  432
Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu
    130                 135                 140
tcc acc tac tac cag gat cag ctg gat ccc ctg gat gag gct cag ctg  480
Ser Thr Tyr Tyr Gln Asp Gln Leu Asp Pro Leu Asp Glu Ala Gln Leu
145                 150                 155                 160
gac aag gca acc gtc cgc ctg atg gcg aag gtt ccg atg ctg gct gca  528
Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala
                165                 170                 175
tac gca cac cgt gcc cgc aag ggt gcg ccg tac atg tac ccg gac aac  576
Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn
            180                 185                 190
tcc ctc aat gcc cgt gag aac ttc ctg cgc atg atg ttc ggt tac ccg  624
Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro
        195                 200                 205
acc gag ccg tac gag gtt gat ccg atc atg gtc aaa gcc ctc gac aag  672
Thr Glu Pro Tyr Glu Val Asp Pro Ile Met Val Lys Ala Leu Asp Lys
```

```
    210                 215                 220
ctg ctc atc ctg cac gca gac cac gag cag aac tgc tcc acc tcc act   720
Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr
225                 230                 235                 240
gtc cgc atg atc ggc tcc gcg cag gcg aac atg ttc gtc tcc atc gcc   768
Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala
                245                 250                 255
ggc ggc atc aac gca ctc tcc ggc ccg ctg cac ggt ggc gcc aac cag   816
Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln
            260                 265                 270
gct gtc ctc gag atg ctc gag gag atc gca gcc aac ggc ggc gac gca   864
Ala Val Leu Glu Met Leu Glu Glu Ile Ala Ala Asn Gly Gly Asp Ala
        275                 280                 285
acc gac ttc atg aac cgc gtg aag aac aag gag aag ggt gtc cgc ctc   912
Thr Asp Phe Met Asn Arg Val Lys Asn Lys Glu Lys Gly Val Arg Leu
    290                 295                 300
atg ggc ttc gga cac cgc gtc tac aag aac tac gat ccg cgt gca gcc   960
Met Gly Phe Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala
305                 310                 315                 320
atc gtc aag gac acc gcc cac gag atc ctc gag cac ctc ggt ggc gac  1008
Ile Val Lys Asp Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp
                325                 330                 335
cca ctg ctg gat ctg gct ctc aag ctg gaa gaa atc gca ctc aac gac  1056
Pro Leu Leu Asp Leu Ala Leu Lys Leu Glu Glu Ile Ala Leu Asn Asp
            340                 345                 350
gat tac ttc atc tcc cgc aag ctg tac ccg aac gtg gac ttc tac acc  1104
Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr
        355                 360                 365
ggc ctg atc tac cgc gcc atg ggc ttc ccg acg gac ttc ttc acc gtc  1152
Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val
    370                 375                 380
ctg ttc gcc atc ggc cgc ctc ccg ggc tgg atc gcc cac tac cgc gag  1200
Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu
385                 390                 395                 400
cag ctc gcc gat ccg ggc gcc aag atc aac cgt cct cgc cag atc tac  1248
Gln Leu Ala Asp Pro Gly Ala Lys Ile Asn Arg Pro Arg Gln Ile Tyr
                405                 410                 415
acc ggt gag acc gca cgc aag atc atc ccc cgc gaa gag cgc tag      1293
Thr Gly Glu Thr Ala Arg Lys Ile Ile Pro Arg Glu Glu Arg
            420                 425                 430
```

<210> 90
<211> 430

<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 90

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Val Ala Ser Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu
  1               5                  10                  15
Phe Glu Met Gly Ile Lys Gln Ala Thr Glu Gly Asn Ser Gly Val Ile
            20                  25                  30
Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly
        35                  40                  45
Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly
    50                  55                  60
Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala
65                  70                  75                  80
Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Lys Gly Glu
                85                  90                  95
Leu Pro Thr Pro Glu Glu Leu His Lys Phe Asn Asp Glu Ile Arg His
            100                 105                 110
His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro
        115                 120                 125
Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu
    130                 135                 140
Ser Thr Tyr Tyr Gln Asp Gln Leu Asp Pro Leu Asp Glu Ala Gln Leu
145                 150                 155                 160
Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala
                165                 170                 175
Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn
            180                 185                 190
Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro
        195                 200                 205
Thr Glu Pro Tyr Glu Val Asp Pro Ile Met Val Lys Ala Leu Asp Lys
    210                 215                 220
Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr
225                 230                 235                 240
Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala
                245                 250                 255
Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln
            260                 265                 270
Ala Val Leu Glu Met Leu Glu Glu Ile Ala Ala Asn Gly Gly Asp Ala
        275                 280                 285
Thr Asp Phe Met Asn Arg Val Lys Asn Lys Glu Lys Gly Val Arg Leu
    290                 295                 300
Met Gly Phe Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala
```

305 310 315 320
Ile Val Lys Asp Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp
325 330 335
Pro Leu Leu Asp Leu Ala Leu Lys Leu Glu Glu Ile Ala Leu Asn Asp
340 345 350
Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr
355 360 365
Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val
370 375 380
Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu
385 390 395 400
Gln Leu Ala Asp Pro Gly Ala Lys Ile Asn Arg Pro Arg Gln Ile Tyr
405 410 415
Thr Gly Glu Thr Ala Arg Lys Ile Ile Pro Arg Glu Glu Arg
420 425 430

<210> 91
<211> 1314
<212> DNA
<213> Brevibacterium lactofermentum

<220>
<221> CDS
<222> (1)..(1311)

<400> 91
atg ttt gaa agg gat atc gtg gct act gat aac aac aag gct gtc ctg 48
Met Phe Glu Arg Asp Ile Val Ala Thr Asp Asn Asn Lys Ala Val Leu
1 5 10 15
cac tac ccc ggt ggc gag ttc gaa atg gac atc atc gag gct tct gag 96
His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile Ile Glu Ala Ser Glu
20 25 30
ggt aac aac ggt gtt gtc ctg ggc aag atg ctg tct gag act gga ctg 144
Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu Ser Glu Thr Gly Leu
35 40 45
atc act ttt gac cca ggt tat gtg agc act ggc tcc acc gag tcg aag 192
Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys
50 55 60
atc acc tac atc gat ggc gat gcg gga atc ctg cgt tac cgc ggc tat 240
Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr
65 70 75 80
gac atc gct gat ctg gct gag aat gcc acc ttc aac gag gtt tct tac 288
Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr

```
                                85                  90                  95
cta ctt atc aac ggt gaa cta cca acc cca gat gag ctt cac aag ttt   336
Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp Glu Leu His Lys Phe
            100                 105                 110
aac gac gag att cgc cac cac acc ctt ctg gac gag gac ttc aag tcc   384
Asn Asp Glu Ile Arg His His Thr Leu Leu Asp Glu Asp Phe Lys Ser
        115                 120                 125
cag ttc aac gtg ttc cca cgc gac gct cac cca atg gca acc ttg gct   432
Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro Met Ala Thr Leu Ala
    130                 135                 140
tcc tcg gtt aac att ttg tct acc tac tac cag gat cag ctg aac cca   480
Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro
145                 150                 155                 160
ctc gat gag gca cag ctt gat aag gca acc gtt cgc ctc atg gca aag   528
Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val Arg Leu Met Ala Lys
                165                 170                 175
gtt cca atg ctg gct gcg tac gca cac cgc gca cgc aag ggt gct cct   576
Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala Arg Lys Gly Ala Pro
            180                 185                 190
tac atg tac cca gac aac tcc ctc aac gcg cgt gag aac ttc ctg cgc   624
Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg
        195                 200                 205
atg atg ttc ggt tac cca acc gag cca tac gag atc gac cca atc atg   672
Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met
    210                 215                 220
gtc aag gct ctg gac aag ctg ctc atc ctg cac gct gac cac gag cag   720
Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His Ala Asp His Glu Gln
225                 230                 235                 240
aac tgc tcc acc tcc acc gtt cgt atg atc ggt tcc gca cag gcc aac   768
Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly Ser Ala Gln Ala Asn
                245                 250                 255
atg ttt gtc tcc atc gct ggt ggc atc aac gct ctg tcc ggc cca ctg   816
Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu
            260                 265                 270
cac ggt ggc gca aac cag gct gtt ctg gag atg ctc gaa gac atc aag   864
His Gly Gly Ala Asn Gln Ala Val Leu Glu Met Leu Glu Asp Ile Lys
        275                 280                 285
aac aac cac ggt ggc gac gca acc gcg ttc atg aac aag gtc aag aac   912
Asn Asn His Gly Gly Asp Ala Thr Ala Phe Met Asn Lys Val Lys Asn
    290                 295                 300
aag gaa gac ggc gtc cgc ctc atg ggc ttc gga cac cgc gtt tac aag   960
Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly His Arg Val Tyr Lys
305                 310                 315                 320
```

```
aac tac gat cca cgt gca gca atc gtc aag gag acc gca cac gag atc   1008
Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu Thr Ala His Glu Ile
                325                 330                 335
ctc gag cac ctc ggt ggc gac gat ctt ctg gat ctg gca atc aag ctg   1056
Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu
            340                 345                 350
gaa gaa att gca ctg gct gat gat tac ttc atc tcc cgc aag ctc tac   1104
Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr
        355                 360                 365
ccg aac gta gac ttc tac acc ggc ctg atc tac cgc gca atg ggc ttc   1152
Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe
    370                 375                 380
cca act gac ttc ttc acc gta ttg ttc gca atc ggt cgt ctg cca gga   1200
Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile Gly Arg Leu Pro Gly
385                 390                 395                 400
tgg atc gct cac tac cgc gag cag ctc ggt gca gca ggc aac aag atc   1248
Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile
                405                 410                 415
aac cgc cca cgc cag gtc tac acc ggc aag gaa tcc cgc aag ttg gtt   1296
Asn Arg Pro Arg Gln Val Tyr Thr Gly Lys Glu Ser Arg Lys Leu Val
            420                 425                 430
cct cgc gag gag cgc taa                                          1314
Pro Arg Glu Glu Arg
        435
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<210> 92
<211> 437
<212> PRT
<213> Brevibacterium lactofermentum

<400> 92

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Met Phe Glu Arg Asp Ile Val Ala Thr Asp Asn Asn Lys Ala Val Leu
  1               5                  10                  15
His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile Ile Glu Ala Ser Glu
            20                  25                  30
Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu Ser Glu Thr Gly Leu
        35                  40                  45
Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys
    50                  55                  60
Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr
65                  70                  75                  80
Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr
                85                  90                  95
```

Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp Glu Leu His Lys Phe
100 105 110
Asn Asp Glu Ile Arg His His Thr Leu Leu Asp Glu Asp Phe Lys Ser
115 120 125
Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro Met Ala Thr Leu Ala
130 135 140
Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro
145 150 155 160
Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val Arg Leu Met Ala Lys
165 170 175
Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala Arg Lys Gly Ala Pro
180 185 190
Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg
195 200 205
Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met
210 215 220
Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His Ala Asp His Glu Gln
225 230 235 240
Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly Ser Ala Gln Ala Asn
245 250 255
Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu
260 265 270
His Gly Gly Ala Asn Gln Ala Val Leu Glu Met Leu Glu Asp Ile Lys
275 280 285
Asn Asn His Gly Gly Asp Ala Thr Ala Phe Met Asn Lys Val Lys Asn
290 295 300
Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly His Arg Val Tyr Lys
305 310 315 320
Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu Thr Ala His Glu Ile
325 330 335
Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu
340 345 350
Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr
355 360 365
Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe
370 375 380
Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile Gly Arg Leu Pro Gly
385 390 395 400
Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile
405 410 415
Asn Arg Pro Arg Gln Val Tyr Thr Gly Lys Glu Ser Arg Lys Leu Val
420 425 430
Pro Arg Glu Glu Arg

435

<210> 93
<211> 1656
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (309)..(1595)

<400> 93
acgcccgatt cttcaacact atcgaagagg tcccaaccca cgcgttgacc cagggcttgg 60
gtacttgtc ccgcgcgcaa aatatcgtgt tggtggcaac tggccaagga aaagcagaca 120
gccatccgcg gaactgtgga aggtccagtg actgcttctt gcccaggttc cattctgcaa 180
atgcacaaca acgccaccat catcgttgat gaagcagcag catccaagct gaaaaatgct 240
gaccattacc gtctcatgga gcaattaaag ctgcgctaga aacaaaaagg aaagtactgt 300
gtggggct atg cac aca gaa ctt tcc agt ttg cgc cct gcg tac cat gtg 350
Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val
1 5 10
act cct ccg cag ggc aga ctc aat gat ccc aat gga atg tac gtc gat 398
Thr Pro Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp
15 20 25 30
gga gat acc ctc cac gtc tac tac cag cac gat cca ggt ttc ccc ttc 446
Gly Asp Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe
35 40 45
gca cca aag cgc acc ggt tgg gct cac acc acc acg ccg ttg acc gga 494
Ala Pro Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly
50 55 60
ccg cag cga ttg cag tgg acg cac ctg ccc gat gct ctt tac ccg gat 542
Pro Gln Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp
65 70 75
gta tcc tat gac ctg gat gga tgc tat tcc ggc gga gcc gta ttt tct 590
Val Ser Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser
80 85 90
gac ggc acg ctt aaa ctt ttc tac acc ggc aac cga aaa att gac ggc 638
Asp Gly Thr Leu Lys Leu Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly
95 100 105 110
aag cgc cgc gcc acc caa aac ctc gtc gaa gtc gag gac cca act ggg 686
Lys Arg Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly
115 120 125
ctg atg ggc ggc att cat cgc cgc tcg cct aaa aat ccg ctt atc gac 734
Leu Met Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp

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                130                 135                 140
gga ccc gcc agc ggt ttt acg ccc cac tac cgc gat ccc atg atc agc   782
Gly Pro Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser
        145                 150                 155
cct gat ggg gat ggt tgg aag atg gtt ctt ggg gct cag cgc gaa aac   830
Pro Asp Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn
    160                 165                 170
ctc acc ggt gca gcg gtt cta tac cgc tcg gca gat ctt gaa aac tgg   878
Leu Thr Gly Ala Ala Val Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp
175                 180                 185                 190
gaa ttc tcc ggt gaa atc acc ttt gac ctc agc gac gca caa cct ggt   926
Glu Phe Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly
                195                 200                 205
tct gcc cct gat ctc gtt cct ggc ggc tac atg tgg gaa tgc ccc aac   974
Ser Ala Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn
            210                 215                 220
ctt ttt acg ctt cgc gat gaa aaa acc ggc gaa gac ctc gat gtg ctg  1022
Leu Phe Thr Leu Arg Asp Glu Lys Thr Gly Glu Asp Leu Asp Val Leu
        225                 230                 235
att ttc tgt cca caa gga ttg gac cgt atc gat gat gag gtt act cac  1070
Ile Phe Cys Pro Gln Gly Leu Asp Arg Ile Asp Asp Glu Val Thr His
    240                 245                 250
tac gca agc tct gac cag tgc gga tat gtc gtc ggc aag ctt gaa gaa  1118
Tyr Ala Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Glu
255                 260                 265                 270
acg acc ttc cgt gtc ctg cga gga ttc agc gag ctg gat ttc ggt cat  1166
Thr Thr Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His
                275                 280                 285
gaa ttc tac gcg ccg cag gtt gca gtc aac ggt tcc gat gcc tgg ctt  1214
Glu Phe Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu
            290                 295                 300
gtg ggc tgg atg gga ttg cct gca cag gat gat cac cca aca gtt gcg  1262
Val Gly Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala
        305                 310                 315
cag gaa gga tgg gtg cac tgc ctg acc gtt cct cgc agg ctt cat ttg  1310
Gln Glu Gly Trp Val His Cys Leu Thr Val Pro Arg Arg Leu His Leu
    320                 325                 330
cgt aac cat gcg atc tat caa gag ctt ctt ctc cca gaa ggg gag tcg  1358
Arg Asn His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser
335                 340                 345                 350
ggg gta act aga tct gta tta ggt tct gaa cct gtc cga gta gac atc  1406
Gly Val Thr Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile
                355                 360                 365
```

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cga gac aat gtt tcc ctc gag tgg gat ggt gtc cgg ttg tct gtg gat   1454
Arg Asp Asn Val Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp
            370                 375                 380
cgc gat ggc gat cgt cgt gta gct gaa gta aaa cct ggc gaa tta gtg   1502
Arg Asp Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val
        385                 390                 395
atc gcg gac gat aat aca gcg att gag ata aca gca ggt cat ggc cag   1550
Ile Ala Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly His Gly Gln
    400                 405                 410
gtt tcc ttc gct ttc cgc acc ttc aaa ggt gac act att gag aga       1595
Val Ser Phe Ala Phe Arg Thr Phe Lys Gly Asp Thr Ile Glu Arg
415                 420                 425
taagtcataa aaaagggcct tctgtggcgg attgtacaaa tacttcgcaa aatcccttga 1655
t                                                                 1656
```

<210> 94
<211> 429
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 94

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Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro
 1               5                  10                  15
Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp
            20                  25                  30
Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro
        35                  40                  45
Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln
    50                  55                  60
Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser
65                  70                  75                  80
Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly
                85                  90                  95
Thr Leu Lys Leu Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg
            100                 105                 110
Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met
        115                 120                 125
Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro
    130                 135                 140
Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp
145                 150                 155                 160
Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr
                165                 170                 175
```

Gly Ala Ala Val Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe
180 185 190
Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala
195 200 205
Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe
210 215 220
Thr Leu Arg Asp Glu Lys Thr Gly Glu Asp Leu Asp Val Leu Ile Phe
225 230 235 240
Cys Pro Gln Gly Leu Asp Arg Ile Asp Asp Glu Val Thr His Tyr Ala
245 250 255
Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Glu Thr Thr
260 265 270
Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe
275 280 285
Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly
290 295 300
Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Gln Glu
305 310 315 320
Gly Trp Val His Cys Leu Thr Val Pro Arg Arg Leu His Leu Arg Asn
325 330 335
His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val
340 345 350
Thr Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Asp
355 360 365
Asn Val Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Asp
370 375 380
Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala
385 390 395 400
Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly His Gly Gln Val Ser
405 410 415
Phe Ala Phe Arg Thr Phe Lys Gly Asp Thr Ile Glu Arg
420 425

<210> 95
<211> 35
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying scrB gene

<400> 95
gtacatattg tcgttagaac gcgtaatacg actca 35

<210> 96
<211> 35
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying scrB gene

<400> 96
cgttagaacg cgtaatacga ctcactatag ggaga 35

<210> 97
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for LA cloning of scrB

<400> 97
gtaaagagcg tcgggcaggt gcgtccactg 30

<210> 98
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for LA cloning of scrB

<400> 98
ggtgtgagcc cagccggtgc gctttggtgc 30

<210> 99

<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for
LA cloning of scrB

<400> 99
atcagccctg atggtgatgg ttggaaaatg 30

<210> 100
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for
LA cloning of scrB gene

<400> 100
ggtgcagcgg ttctataccg ctcgacagat 30

<210> 101
<211> 32
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for
amplifying scrB gene

<400> 101
ggcccgggac gcccgattct tcaacactat cg 32

<210> 102
<211> 32
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying scrB gene

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<210> 103
<211> 30
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer for amplifying icd gene

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<210> 104
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
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<210> 105
<211> 32
<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer for amplifying gdh gene

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<210> 106
<211> 32
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<213> Artificial Sequence

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<210> 107
<211> 30
<212> DNA

<213> Artificial Sequence

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<210> 108
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<213> Artificial Sequence

<220>
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<400> 108
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